

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:20:08 ; Search time 60 Seconds
(without alignments)
998.335 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLLWLLFLVTAHSLCQPG.....ENGIPSDPLDMKGILMXPFS 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1102	100.0	212	3	AAY66751 Membrane-
2	1102	100.0	212	3	AAB33447 Human PRO
3	1102	100.0	212	3	AAB24430 Human PRO
4	1102	100.0	212	4	AU12412 Human PRO
5	1102	100.0	212	4	AAB5274 Human PRO
6	1102	100.0	212	6	ABU58089 Human PRO
7	1102	100.0	212	6	ABU59167 Novel hum
8	1102	100.0	212	6	ABU82679 Human sec
9	1102	100.0	212	6	ABO17856 Novel hum
10	1102	100.0	212	6	ABU60598 Human sec
11	1102	100.0	212	6	ABU13980 Human PRO
12	1102	100.0	212	6	ABU81110 Human PRO
13	1102	100.0	212	6	ABU72565 Novel hum
14	1102	100.0	212	6	ABU66810 Human PRO
15	1102	100.0	212	6	ABU59891 Novel sec
16	1102	100.0	212	6	ABU59314 Human sec
17	1102	100.0	212	6	ABO26011 Human PRO
18	1102	100.0	212	6	ABO25081 Human sec
19	1102	100.0	212	6	ABU59020 Human sec
20	1102	100.0	212	6	ABU92398 Novel hum
21	1102	100.0	212	6	ABU59463 Novel hum
22	1102	100.0	212	6	ABU67086 Human sec
23	1102	100.0	212	6	ABU92229 Novel hum
24	1102	100.0	212	6	ABU10935 Human PRO
25	1102	100.0	212	6	ABU81687 Novel hum

ALIGNMENTS

RESULT 1

AAY66751
ID AAY66751 standard; protein; 212 AA.

XX AC AAY66751;

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO1312.

XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX XW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX PN WO9963088-A2.

XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99WO-US012252.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 04-JUN-1998; 98US-0088326P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 05-JUN-1998; 98US-0088555P.

XX PR 10-JUN-1998; 98US-0088722P.

XX PR 10-JUN-1998; 98US-0088730P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

XX PR 10-JUN-1998; 98US-0088740P.

XX PR 10-JUN-1998; 98US-0088741P.

XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

26 1102 100.0 212 6 ABU88626 Human sec
27 1102 100.0 212 6 ABO34140 Human PRO
28 1102 100.0 212 6 ADA46001 Novel hum
29 1102 100.0 212 6 ADA76432 Human PRO
30 1102 100.0 212 6 ADA19082 Human PRO
31 1102 100.0 212 6 ADA61705 Homo sapi
32 1102 100.0 212 6 ADB19490 Novel hum
33 1102 100.0 212 6 ADB28031 Human PRO
34 1102 100.0 212 6 ADA86510 Novel hum
35 1102 100.0 212 6 ADB16074 Human PRO
36 1102 100.0 212 6 ADA37898 Human sec
37 1102 100.0 212 6 ADA47860 Human PRO
38 1102 100.0 212 6 ADA21584 Human sec
39 1102 100.0 212 6 ADA10371 Human PRO
40 1102 100.0 212 6 ADA67655 Human PRO
41 1102 100.0 212 6 ADB30662 Human PRO
42 1102 100.0 212 6 ADA85958 Novel hum
43 1102 100.0 212 6 ADA17915 Human PRO
44 1102 100.0 212 6 ADA97170 Human PRO
45 1102 100.0 212 6 ADA79474 Human PRO

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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0088909P.
PR 12-JUN-1998; 98US-0089103P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090433P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090533P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091628P.
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PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 12-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096943P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

( GETH ) GENENTECH INC.
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR N-PSDE; AAZ65097.
XX Membrane-bound proteins and related nucleotide sequences.
PT Claim 12; Fig 278; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX Sequence 212 AA;
SQ Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5,8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLMLPFLVTAIAELCQPGAENAFKVRSLRIRALGDKAYADNTNEEYLFKAMVAFSMRK 60
Db 1 MLMLPFLVTAIAELCQPGAENAFKVRSLRIRALGDKAYADNTNEEYLFKAMVAFSMRK 60

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QY 61 VFNREATEISHVLLCNVTQVSFWFVVTDPDSKXHTLPAVEVQSAIPMKNRINNAPFLND 120
DB 61 VFNREATEISHVLLCNVTQVSFWFVVTDPDSKXHTLPAVEVQSAIPMKNRINNAPFLND 120
QY 121 QTLFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
DB 121 QTLFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 2
AAB33447
ID AAB33447 standard; protein; 212 AA.
AC AAB33447;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO1312 protein UNQ678 SEQ ID NO:161.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;
XX haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
XX antianaemic; hepatotropic; virucide; antipoxiatic; anti allergic;
XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
XX osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX autoimmune thrombocytopaenia; immune-mediated renal disease;
XX demyelinating disease; hepatobiliary disease; Whipple's disease;
XX inflammatory bowel disease; gluten-sensitive enteropathy;
XX autoimmune disease; immune-mediated skin disease; allergic disease;
XX immunological disease; immun-mediated skin disease; allergic disease;
XX graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WC200053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005841.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.

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PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028585.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
XX WPI; 2000-572271/53.
XX N-PSDB; AAC58612.
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 68; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
XX be used in the treatment of immune related diseases. The human PRO
XX proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX treating and diagnosing immune related disorders. The disorders are
XX selected from systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases, inflammatory bowel
XX disease, peripheral nervous systems, hepatobiliary diseases, inflammatory
XX disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
XX or immune-mediated skin diseases, allergic diseases, immunological
XX diseases of the lung, and transplantation associated diseases including
XX graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
XX represent PCR primers and hybridisation probes used in the isolation of
XX human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
XX represent human PRO polynucleotide and protein sequences given in the
XX exemplification of the present invention
XX
XX Sequence 212 AA;
XX
XX Query Match 100.0%; Score 1102; DB 3; Length 212;
XX Best Local Similarity 100.0%; Pred. NO. 5.8e-114;
XX Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLWLLPFLVTAHAEIQCQGAENAFKVRISIRTLGDKAYAWDTNEEYLFKAWAFSMRK 60
XX DB 1 MLWLLPFLVTAHAEIQCQGAENAFKVRISIRTLGDKAYAWDTNEEYLFKAWAFSMRK 60
XX
XX QY 61 VFNREATEISHVLLCNVTQVSFWFVVTDPDSKXHTLPAVEVQSAIPMKNRINNAPFLND 120
XX DB 61 VFNREATEISHVLLCNVTQVSFWFVVTDPDSKXHTLPAVEVQSAIPMKNRINNAPFLND 120
XX
XX QY 121 QTLFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
XX DB 121 QTLFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
XX
XX QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
XX DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
XX
XX RESULT 3

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AA824430
ID AAB24430 standard; protein; 212 AA.
XX AAB24430;
XX 07-NOV-2000 (first entry)
XX Human PRO1312 protein sequence SEQ ID NO:214.
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
XX diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
XX angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
XX cytotatic; gene therapy; vaccine.
XX Homo sapiens.
XX WO200032221-A2.
XX 08-JUN-2000.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1998; 98WO-US025108.
XX 16-DEC-1998; 98US-0112850P.
XX 12-JAN-1999; 99US-0115554P.
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
XX Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
XX Smith V, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-412154/35.
XX N-PSDB; AA77680.
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
XX and treating diagnosing a cardiovascular, endothelial or angiogenic
XX disorders in mammals.
XX Claim 72; Fig 86; 315pp; English.
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating diagnosing a
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the prevention,
XX treatment and diagnosis of diseases associated with inappropriate PRO
XX expression such as cardiovascular, endothelial or angiogenic disorders in
XX mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
XX example, the nucleic acids (NCs) and vectors containing them and the PRO
XX polypeptide may be used to treat disorders associated with decreased PRO
XX expression. AA77510 to AA77721 and AA824388 to AA824435 represent
XX nucleotide and protein sequences used in the exemplification of the
XX present invention
XX Sequence 212 AA;
XX

Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114; Indels 0; Gaps 0;
Matches 212; Conservative 0; Mismatches 0;
Qy 1 MLWLLPFLVTAIHAELCQPGAENAFKVRISIRTAIGDKAYADTNEYLFKAMVAFSMRK 60
Db 1 MLWLLPFLVTAIHAELCQPGAENAFKVRISIRTAIGDKAYADTNEYLFKAMVAFSMRK 60
Qy 61 VPREATEISHVLICNVTVQVSVFVVDPSKNETLPAVEVQSAIRNMKNRINNAPFLND 120
Db 61 VPREATEISHVLICNVTVQVSVFVVDPSKNETLPAVEVQSAIRNMKNRINNAPFLND 120
Qy 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRERKNKPSYVD 180
Db 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRERKNKPSYVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
RESULT 4
AAU12412
ID AAU12412 standard; protein; 212 AA.
AC AAU12412;
XX 24-OCT-2001 (first entry)
DT Human PRO1312 polypeptide sequence.
DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; factor VIIa; gene therapy.
XX Homo sapiens.
XX WO200140466-A2.
XX 07-JUN-2001.
XX 01-DEC-2000; 2000WO-US032678.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 09-DEC-1999; 99US-0170262P.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 30-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005641.
XX 03-MAR-2000; 2000US-0187202P.
XX 10-MAR-2000; 2000WO-US006319.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.

CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
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DB 61 VPNEATEISHVLLCNVTQRVSFWFVTDPSKNHTLPAVEVQSARINNNKFINNAFLND 120

QY 121 QTLFPLKIPSTLAPDPSPVPIIIFGVIFCIIVAIALLISIQWRRKKNKEPSEVD 180
DB 121 QTLFPLKIPSTLAPDPSPVPIIIFGVIFCIIVAIALLISIQWRRKKNKEPSEVD 180

QY 181 DAEDKCNMTTENGIPSDPLDMKGGILMMP 212
DB 181 DAEDKCNMTTENGIPSDPLDMKGGILMMP 212

RESULT 6
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AC ABU58089;
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DT 14-APR-2003 (first entry)
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KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ABEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
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PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
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PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 23-AUG-2000; 2000WO-US023522.
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XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NP,
XX Roy MA, Stewart RA, Tumas D, Watanabe CK, Williams PM, Wood WL,
XX Zhang Z;
XX WPI; 2003-247083/24.
XX N-PSDB; ABX80370.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments.
XX Claim 12; Fig 278; 648pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce C-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and antagonist of this polypeptide are
XX useful for treating cancerous tumours. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing
XX immune response. PRO826, PRO1068 or PRO1132 enhance survival of
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of
XX rod photoreceptor cells) and therefore are useful for treating retinal
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,
XX and therefore are useful for treating kidney disorders associated with
XX decreased mesangial cell function such as Berger disease or other
XX nephropathies associated with dermatitis, herpetiformis or Crohn's
XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
XX proliferation and/or redifferentiation of chondrocytes in culture and are
XX thus useful for treating sports injuries, and arthritis. This is the
XX amino acid sequence of a novel human PRO protein
XX Sequence 212 AA;
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Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWLLFLVTAIHAELCPGNAFKVRLSIRLTALGDKAYAWDTNNEVLFKAWAFMRK 60
DB 1 MLWLLFLVTAIHAELCPGNAFKVRLSIRLTALGDKAYAWDTNNEVLFKAWAFMRK 60
QY 61 VPNEEATEISHVLLCNVQVSFWVWTDPSKNHTLPAVEVQSAIRMKNNKINNAFFLND 120
DB 61 VPNEEATEISHVLLCNVQVSFWVWTDPSKNHTLPAVEVQSAIRMKNNKINNAFFLND 120
QY 121 QTLEFLKIPSTLAPMDSPVPIIIFGVITFCIIIVAILLILSGIWRORAKNEPSSVD 180
DB 121 QTLEFLKIPSTLAPMDSPVPIIIFGVITFCIIIVAILLILSGIWRORAKNEPSSVD 180
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Db 121 QTLFLKIPSTLAPMPDSVPVWIIIFGVIFCIIVAIALLILSGINQRRKNKEPSEVD 180
 Qy 181 DAEDKCNMTIENGIPSDPLDMKGGLMPS 212
 Db 181 DAEDKCNMTIENGIPSDPLDMKGGLMPS 212
 RESULT 8
 ABUS2679
 ID ABUS2679 standard; protein; 212 AA.
 AC ABUS2679;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1312.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosa; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003032023-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 14-NOV-2001; 2001US-00590711.
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 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
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 PR 07-MAY-1998; 98US-0084600P.
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 PR 02-JUN-1998; 98US-0087607P.
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 PR 03-JUN-1998; 98US-0087827P.
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 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
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 PR 04-JUN-1998; 98US-0088036P.
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 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
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 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
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 PR 04-AUG-1998; 98US-0095285P.
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 PR 17-AUG-1998; 98US-0096897P.

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PR	31-AUG-1998;	98US-0098525P.	DB			
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PR	16-DEC-1999;	98US-0158663P.	DB			
PR	20-DEC-1999;	98US-0158663P.	QY			
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PR	11-FEB-2000;	2000US-0000213P.	DB			
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 Best Local Similarity 100.0%; Pred. No. 5.8e-114;
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PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028554.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 13-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
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PR 14-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
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PR 05-JUN-2001; 2001US-00874503.
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PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

XX WPI; 2003-341980/32.
XX N-PSDB; ACD24093.
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
XX syndrome (AIDS), or cancer.
XX Claim 12; Fig 482; 660pp; English.
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5 8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 DAEDKCNMTIENGIPSDPLDMKGILMPS 212
RESULT 10
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AC ABU0598;
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XX 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein, #157.
XX Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX diagnostic; therapeutic; gene therapy.
XX Homo sapiens.
XX US2002160384-A1.
PN

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XX PD 31-OCT-2002.
XX PF 14-NOV-2001; 2001US-0092598.
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-US020066.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0075910P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088022P.
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XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 04-JUN-1998; 98US-0088126P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088742P.
XX PR 10-JUN-1998; 98US-0088810P.
XX PR 10-JUN-1998; 98US-0088824P.
XX PR 10-JUN-1998; 98US-0088826P.
XX PR 11-JUN-1998; 98US-0088858P.
XX PR 11-JUN-1998; 98US-0088861P.
XX PR 11-JUN-1998; 98US-0088876P.
XX PR 12-JUN-1998; 98US-0089105P.
XX PR 16-JUN-1998; 98US-0089440P.
XX PR 16-JUN-1998; 98US-0089512P.
XX PR 16-JUN-1998; 98US-0089514P.
XX PR 17-JUN-1998; 98US-0089532P.
XX PR 17-JUN-1998; 98US-0089538P.
XX PR 17-JUN-1998; 98US-0089598P.
XX PR 17-JUN-1998; 98US-0089599P.
XX PR 17-JUN-1998; 98US-0089600P.
XX PR 17-JUN-1998; 98US-0089653P.
XX PR 18-JUN-1998; 98US-0089801P.
XX PR 18-JUN-1998; 98US-0089907P.
XX PR 18-JUN-1998; 98US-0089908P.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 07-OCT-1998; 98WO-US021141.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 05-JAN-1999; 99WO-US000106.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 30-NOV-1999; 99WO-US028813.
XX PR 01-DEC-1999; 99WO-US0288301.
XX PR 01-DEC-1999; 99WO-US028834.
XX PR 16-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.

22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
02-MAR-2000; 2000WO-US005004.
04-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.

(GRTH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kijavini JJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;

WPI: 2003-288106/28.
N-PSDB; ABX90348.

New transmembrane polypeptides and nucleic acids encoding the
polypeptides, useful in gene therapy, in chromosome identification, as
chromosome markers, or in generating probes.

Claim 12; Fig 278; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides
comprising a sequence without signal peptide and the nucleic acid
encoding them. The polypeptides can be used to raise antibodies that
specifically bind to the PRO polypeptide, for linking a bioactive
molecule to a cell expressing a PRO protein and for modulating at least
one biological activity of a cell. The PRO polypeptides or
polynucleotides are also useful in gene therapy, in chromosome
identification, as chromosome markers, or in generating probes. The PRO
polypeptides are useful as molecular markers for protein electrophoresis,
and the isolated nucleic acids may be used for recombinantly expressing
those markers. The PRO polypeptides and nucleic acids may also be used in
tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
PRO, and in affinity purification of PRO from recombinant cell culture or
natural sources. The sequences presented in AB060478-AB060624 are the PRO
polynucleotides of the invention. Note: The sequence data for this patent
is also available in electronic format from USPTO at
segdata.uspto.gov/sequence.html

SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMLFLFLVTAHAEICQPCAEAFKVRISITLGDKAYADTNEEYLFKAMVAFSMRK 60
DB 1 MLMLFLFLVTAHAEICQPCAEAFKVRISITLGDKAYADTNEEYLFKAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTORVSFWFVVTDPDSKRHILPAVEVOSATRMKRNINAFPLND 120

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CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/psipdIDentry.html
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.8e-114;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMLLPELVTAHAEICOPGNAFKVLSIRLTALGDKAYADTNEEYLFKAMVAFSRK 60
 Db 1 MMLLEFFLVTAHAEICOPGNAFKVLSIRLTALGDKAYADTNEEYLFKAMVAFSRK 60
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 Db 61 VPREATEISHVLLCNVTRQVSFWVTPDSKNHTLPAVEQSAIRNMKNINNAFLND 120
 QY 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVICIIIVAILLIGIWORRKNKEPSEVD 180
 Db 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVICIIIVAILLIGIWORRKNKEPSEVD 180
 QY 181 DAEDKCNMTIENGIPSDPLDKGGLMPS 212
 Db 181 DAEDKCNMTIENGIPSDPLDKGGLMPS 212

RESULT 12

ID ABU81110
 XX ABU81110 standard; protein; 212 AA.
 AC ABU31110;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 XX Human PRO polypeptide #241.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnary; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.
 XX Homo sapiens.
 OS
 XX
 XX US2003004311-A1.
 FN
 XX
 XX 02-JAN-2003.
 XX
 XX 19-DEC-2001; 2001US-00028072.
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 XX 18-JUN-1997; 97US-0049911P.
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 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059352P.
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 PR 24-SEP-1997; 97US-0059836P.
 PR 17-OCT-1997; 97US-0062250P.
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 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 16-DEC-1997; 97US-0069694P.
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 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 20-MAR-1998; 98US-0078310P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 31-MAR-1998; 98US-0079728P.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 16-SEP-1998; 98WO-US019177.
 PR 17-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.

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PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 08-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US0003565.
PR 18-FEB-2000; 2000WO-US0004341.
PR 18-FEB-2000; 2000WO-US0004342.
PR 22-FEB-2000; 2000WO-US0004414.
PR 24-FEB-2000; 2000WO-US0004914.
PR 24-FEB-2000; 2000WO-US0005004.
PR 01-MAR-2000; 2000WO-US0005601.
PR 02-MAR-2000; 2000WO-US0005746.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CX, Wood WI, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX N-PSDB; ACA67234.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
XX Claim 12; Fig 482; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. AB08070-AB08114 represent the human PRO
CC polypeptides of the invention. Note: the sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDiEntry.html
XX
XX Sequence 212 AA;
SQ
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLWLLFLVTAIAEELCOPGAENAFKVRISIRIALGDKAYADTNEYLFKAWVAFSMRK 60
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DB 61 VFNREATEISHVLLCNVTVRSFVVTDPSPKXHTLPFAVEVQSAIRMKNNRINNAFFLND 120
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QY 181 DAEDKCNMTIENGIPSPDLDMKGGILMMP 212
DB 181 DAEDKCNMTIENGIPSPDLDMKGGILMMP 212
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RESULT 13
ABU72565
ID ABU72565 standard; protein; 212 AA.
XX
XX AC ABU72565;
XX
XX DT 17-JUN-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO1312.
XX
XX KW Human, secreted and transmembrane protein; cytostatic; anti-HIV;
XX viricide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
XX PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
XX drug screening.
XX
XX OS Homo sapiens.
XX
XX PN US2003003531-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 19-NOV-2001; 2001US-00989734.
XX
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-US020069.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
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XX PR 04-JUN-1998; 98US-0088026P.
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XX PR 12-JUN-1998; 98US-0088876P.
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XX PR 17-JUN-1998; 98US-0089600P.
XX PR 17-JUN-1998; 98US-0089653P.
XX PR 18-JUN-1998; 98US-0089801P.
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PR 20-APR-1999; 99WO-US0008615.
PR 14-MAY-1999; 99WO-US010733.
PR 01-JUN-1999; 99WO-US012252.
PR 02-JUN-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
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PR 11-FEB-2000; 2000WO-US003565.
PR 16-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00794998.
PR 28-FEB-2001; 2001WO-US0006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806899.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
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PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W,
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-232040/31.
XX N-PSDB; ACA03843.
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX Claim 12; Fig 482; 680pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU6570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipdb/entry.html
XX Sequence 212 AA;
XX Query Match 100.0%; Score 1102; DB 6; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-114;
XX Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWLLFFLVTAIHAELCQFGAENAPKVLRSIRTAIGDXYAWDTNBYLFKAMVAFSMRK 60
DB 1 MLWLLFFLVTAIHAELCQFGAENAPKVLRSIRTAIGDXYAWDTNBYLFKAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSALRMKNKRNINNAFFLND 120
DB 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSALRMKNKRNINNAFFLND 120
QY 121 QTLEFLKIPSTLAPMPDPSVPIWIIIFGVIFCIITVAIIALLISGIWQRRRNKPESEVD 180
DB 121 QTLEFLKIPSTLAPMPDPSVPIWIIIFGVIFCIITVAIIALLISGIWQRRRNKPESEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212
RESULT 15
ABU59891
ID ABU59891 standard; protein; 212 AA.
XX ABU59891;
XX ABU59891;
DT 13-MAY-2003 (first entry)
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XX DE Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
XX KW cardiac insufficiency disorder; cancer; tumour; immune response;
XX KW adenal cortical capillary endothelial growth; c-fos induction;
XX KW vascular endothelial growth factor inhibition; VEGF inhibition;
XX KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX KW retinal neurons cell survival; rod photoreceptor cell survival;
XX KW renal disorder; retinitis pigmentosa; kidney disorder;
XX KW mammalian kidney mesangial cell proliferation; Berger disease;
XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX KW chondrocyte redifferentiation; sports injury; arthritis.
OS Homo sapiens.
XX XX
XX PN US2003017563-A1.
XX PD 23-JAN-2003.
XX PF 07-MAY-2002; 2002US-00140808.
XX XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022921.
PR 29-OCT-1998; 98WO-US022922.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 13-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US008566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen MS, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-148238/14.
DR N-PSDB; ABX89381.
DR Two hundred and seventy five nucleic acids encoding PRO polypeptides,
XX useful for treating pericyte-associated tumors, diabetes and various bone
XX and/or cartilage disorders, e.g. arthritis.
XX Claim 12; Fig 482; 659pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLWLLFVLVTAHAELOCPGAEAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFVLVTAHAELOCPGAEAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
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Db 61 VPNEATEISHVLLCNVTQRVSFVFWVTPDPSKNHTLPAVEVQSARIMNKNRINNAPFLND 120
Qy 121 QTLFELKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIATALLSGIMORREKKEPSEVD 180
Db 121 QTLFELKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIATALLSGIMORREKKEPSEVD 180
Qy 181 DAEDKCNWITIENGIPSDPLDMKGILMWPS 212
Db 181 DAEDKCNWITIENGIPSDPLDMKGILMWPS 212

Search completed: April 1, 2004, 16:26:25
Job time : 63 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2004, 16:25:14 ; Search time 22 Seconds
(without alignments)
497.487 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLWLLPFLVTAHAEICQPG.....ENGIPSDPLDMKGGILMPS 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	376	34.1	805	3	US-08-989-299-2
2	376	34.1	805	4	US-10-158-847-142
3	376	34.1	805	4	US-09-407-427-2
4	359	32.6	711	4	US-10-158-847-138
5	289	26.2	681	4	US-10-158-847-140
6	90	8.2	799	1	US-08-188-228-42
7	90	8.2	799	1	US-08-332-638-42
8	89.5	8.1	793	1	US-08-188-228-54
9	89.5	8.1	793	1	US-08-332-643-48
10	89.5	8.1	793	1	US-08-332-638-54
11	88	8.0	363	1	US-07-946-497-7
12	88	8.0	363	1	US-08-483-322-7
13	88	8.0	363	2	US-08-478-882-7
14	86	7.8	503	1	US-07-946-497-2
15	86	7.8	503	1	US-08-483-322-2
16	86	7.8	503	2	US-08-478-882-2
17	84.5	7.7	339	2	US-08-892-880-3
18	83.5	7.6	1337	3	US-08-854-585-2
19	83.5	7.6	1337	4	US-09-447-533-2
20	83.5	7.6	1337	5	PCT-US95-05512-2
21	82.5	7.5	529	4	US-09-134-000C-5948
22	78.5	7.1	438	4	US-09-404-879A-390
23	78.5	7.1	833	4	US-09-404-879A-389
24	78.5	7.1	914	4	US-09-404-879A-312
25	78.5	7.1	914	4	US-09-338-933-312
26	75.5	6.9	944	4	US-09-107-532A-4864
27	75.5	6.9	2035	2	US-08-479-537A-2

28 75.5 6.9 2035 3 US-09-083-116-2 Sequence 2, Appli
29 75.5 6.9 2035 4 US-09-134-916A-2 Sequence 2, Appli
30 75 6.8 1260 3 US-09-245-041-2 Sequence 2, Appli
31 73.5 6.7 298 1 US-08-118-270-76 Sequence 76, Appli
32 73.5 6.7 298 5 PCT-US93-08528-76 Sequence 76, Appli
33 73.5 6.7 562 4 US-09-489-032A-8574 Sequence 8574, Ap
34 73.5 6.7 796 2 US-08-738-343-2 Sequence 2, Appli
35 73 6.6 14 3 US-08-505-223-28 Sequence 28, Appli
36 73 6.6 14 4 US-09-247-155-28 Sequence 28, Appli
37 73 6.6 14 4 US-09-663-600A-28 Sequence 6, Appli
38 73 6.6 14 4 US-09-621-976-6 Sequence 7985, Ap
39 73 6.6 195 4 US-09-543-681A-7985 Sequence 15, Appli
40 72.5 6.6 299 4 US-09-651-200-15 Sequence 136, App
41 72 6.5 283 2 US-08-332-562A-136 Sequence 2146, Ap
42 72 6.5 510 4 US-09-540-236-2148 Sequence 58, Appli
43 71.5 6.5 796 1 US-08-188-228-58 Sequence 52, Appli
44 71.5 6.5 796 1 US-08-332-643-52 Sequence 58, Appli
45 71.5 6.5 796 1 US-08-332-638-58

ALIGNMENTS

RESULT 1
US-08-989-299-2
; Sequence 2, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-299-2

Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;
Qy 19 PCENAFKVLIRIALGDKAYADTNEEYLFKAVAPSMR----KVPNEAT-ELSHVL 73
Db 612 PYADSIKVRISLKGALGKAYEWNDNENYLFSSVAYAMROYFLKVRQNMILFGEDVR 671
Qy 74 LCNVTRQVSFWFWVDPSK-NHTLPAVEVQSAIRNMKNRINNAPFLNDOTLEFLKIPSTL 132


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; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 681
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

Query Match      26.2%; Score 289; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 1.4e-24;
Matches 63; Conservative 23; Mismatches 39; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNNEEYLFKAMVAFNR-----KVPNREAT-EISHVL 73
Db 551 PYADQSIKVRISLKSALGDKAYEMNDNEMYLPESSVAYARQYFLKVKQWILFGEDYR 610

QY 74 LCVNTOVSFWFVVTDPDK-NHTLPAVEVQSALRMKRNINNAFFNDQTLFLKIPSTL 132
Db 611 VANLKPRISFNFFVTAQKVDIIPRTVEVEKAIMRSRINDAPRLNDDSLFLGIQPTL 670

QY 133 APPMDPSVPIW 143
Db 671 GPNQPPVSIW 681

RESULT 6
US-08-188-228-42
; Sequence 42, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 559772sand, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340

; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 681
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
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; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

Query Match      8.2%; Score 90; DB 1; Length 799;
Best Local Similarity 21.4%; Pred. No. 0.2;
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAELCOPGAENAFKVLRSIRLTALGDKAYAWDT-----NNEEYLFKAMVAFNRKVPN 63
Db 432 HTDLERQFNINADGKITLATPLDRELSVWENISIIATEIRNHSQISRPVPAIKVLDV-N 490

QY 64 REATEIS---HVLLC-----NVTORVSFWFVVTDPDKNH-----TLPAVEVQSALRMK 109
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QY 110 RRINNAFL-----NDQTLFLKIPSTLA-----PPMDPSVPIWIIIFG----- 148
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QY 149 -----VFCLIIIVAILLILSGIWOQRKKEPSEVDDAEDKCNMIT 191
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QY 192 IEN 194
Db 667 YDD 669

RESULT 7
US-08-332-638-42
; Sequence 42, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
```

TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 799 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-332-638-42

Query Match 8.2%; Score 90; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 0.2;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAEICQGAENAFKVRISRTALGKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
 DB 432 HTDLERQFNINADGGKITLATPLDRELSVWHNIIATEIRNHSQISRPVPAIKVLDV-N 490
 QY 64 REATEIS---HVLIC-----NVTQVSFWFVTDPSKNH-----TLPVAVQSAIRMNK 109
 DB 491 DNAPEFASYEAFLECGKPGQVIQTVA-MDKDDPKNGHFFLYSLPVMVNNFNFTIKK 549
 QY 110 NRINNAFFL-----NDQTLFLKIPSTLA---PPMDPSVPIMIIIFG----- 148
 DB 550 NEDNSLSILAKHNGFNKQEVYLLPIVISGNNPPLSSTLTIRVCGGNDGVQSCN 609
 QY 149 -----VFCHIIIVAIALLISGIWQRNKKKEPSEVDDAEDKCNMIT 191
 DB 610 VEAYVLPGLSGMALIAILACIILLVIVVLF--VTLRRHKN-EPLTIKDDDEDVRENIIR 666
 QY 192 IEN 194
 DB 667 YDD 669

RESULT 8

US-08-188-228-54
 Sequence 54, Application US/08188228
 Patent No. 559725

GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESS: Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188,228
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,460
 FILING DATE: 19 APR 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 559725 and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31340
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 793 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-188-228-54

Query Match 8.1%; Score 89.5; DB 1; Length 793;
 Best Local Similarity 20.6%; Pred. No. 0.22;
 Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

QY 13 HAEICQGAENAFKVRISRTALGKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
 DB 425 HTDLERQFNINADGGKITLATPLDRELSVWHNIIATEIRNHSQISRPVPAIKVLDV-N 483
 QY 64 REATEIS---HVLIC-----NVTQVSFWFVTDPSKNH-----TLPVAVQSAIRMNK 109
 DB 484 DNAPEFASYEAFLECGKPGQVIQTVA-MDKDDPKNGHFFLYSLPVMVNNFNFTIKK 542
 QY 110 NRINNAFFL-----NDQTLFLKIPSTLA---PPMDPSVPIMIIIFG----- 148
 DB 543 NEDNSLSILAKHNGFNKQEVYLLPIVISGNNPPLSSTLTIRVCGGNDGVQSCN 602
 QY 149 -----VFCHIIIVAIALLISGIWQRNKKKEPSEVDDAEDKCNMIT 191
 DB 603 VEAYVLPGLSGMALIAILACIILLVIVVLF--VTLRRHKN-EPLTIKDDDEDVRENIIR 660
 QY 192 IEN 194
 DB 661 YDD 663

RESULT 9

US-08-332-643-48
 Sequence 48, Application US/08332643
 Patent No. 5639634

GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESS: Bicknell
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,643
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/872,643
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5639634 and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/30795
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-643-48

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. NO. 0.22;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

Qy 13 HAEICQGAENAFKVLRSIRLTALGDKAYAWDT-----NEEYLFKAMVAESMRKVPN 63
Db 425 HTDLERQFNADGGKITLATPLDRELSVMHNITIIATEIRNHSQISRVPVAKVLDV-N 483
Qy 64 REATEIS---HVLIC-----NVTQVSFWFVVTDPKSH-----TLPAVEVQSARMK 109
Db 484 DNAPEFASVEAFLECEKNGKGVQIVTUSA-MDKDDPKNGHYFLYLLPEWVNNPFTIKK 542
Qy 110 NRINNAFFL-----NDQLEFLKIPSTLA-----PPMDESVPIWIIIFG----- 148
Db 543 NEDNSLSILAKHNGFNQRKQEVLLPIIISDSGNPPLSSTLTIRVCGCSNDGVVQSCN 602
Qy 149 -----VFICIIIVATAILLSGIWMRRKKEPSEVDDAEKCNMIT 191
Db 603 VEAYVLPGLSMGALIAILACILLLVIVLPF--VTLRRHQKNEPLIKDDVDRENIIR 660
Qy 192 IEN 194
Db 661 YDD 663

RESULT 10
US-08-332-638-54
; Sequence 54, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.2S
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3885
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-54

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. NO. 0.22;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

Qy 13 HAEICQGAENAFKVLRSIRLTALGDKAYAWDT-----NEEYLFKAMVAESMRKVPN 63
Db 425 HTDLERQFNADGGKITLATPLDRELSVMHNITIIATEIRNHSQISRVPVAKVLDV-N 483
Qy 64 REATEIS---HVLIC-----NVTQVSFWFVVTDPKSH-----TLPAVEVQSARMK 109
Db 484 DNAPEFASVEAFLECEKNGKGVQIVTUSA-MDKDDPKNGHYFLYLLPEWVNNPFTIKK 542
Qy 110 NRINNAFFL-----NDQLEFLKIPSTLA-----PPMDESVPIWIIIFG----- 148
Db 543 NEDNSLSILAKHNGFNQRKQEVLLPIIISDSGNPPLSSTLTIRVCGCSNDGVVQSCN 602
Qy 149 -----VFICIIIVATAILLSGIWMRRKKEPSEVDDAEKCNMIT 191
Db 603 VEAYVLPGLSMGALIAILACILLLVIVLPF--VTLRRHQKNEPLIKDDVDRENIIR 660
Qy 192 IEN 194
Db 661 YDD 663

RESULT 11
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.2S
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 1691S/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
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;
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-946-497-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMPDPSVPIIIFGVIFCIIVAIALLILSGIWQRR-----171
DB 396 VTTTSGPARRPQIPEWII---LASLLALAILAVCIAVNSRRRCGQKKLVNSGNGTV 452
QY 172 KNKPESEVDDADKCNMTIENGIPSD-----PLDMKGGI 207
DB 453 EDRKPSLNGEASKSQEWVHLVKNKEPTETPDQFMTADETRNLQSVDMKIGV 503

RESULT 15
US-08-483-322-2
; Sequence 2, Application us/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERBLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-322-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMPDPSVPIIIFGVIFCIIVAIALLILSGIWQRR-----171
DB 396 VTTTSGPARRPQIPEWII---LASLLALAILAVCIAVNSRRRCGQKKLVNSGNGTV 452
QY 172 KNKPESEVDDADKCNMTIENGIPSD-----PLDMKGGI 207
DB 453 EDRKPSLNGEASKSQEWVHLVKNKEPTETPDQFMTADETRNLQSVDMKIGV 503

Search completed: April 1, 2004, 16:29:00
Job time : 23 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:27:59 ; Search time 41 Seconds
(without alignments)
1356.389 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102

Sequence: 1 MLWLLPFLVTAHAEACQPC.....ENGIPSDPLDMKGGILMPS 212

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Gapop 10.0 , Gapext 0.5

Searched: 1069545 seqs, 262320428 residues

Total number of hits satisfying chosen parameters: 1069545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1102	100.0	212	9	US-09-989-723-387
3	1102	100.0	212	9	US-09-989-279-387
4	1102	100.0	212	9	US-09-989-727-387
5	1102	100.0	212	9	US-09-989-731-387
6	1102	100.0	212	9	US-09-989-732-387
7	1102	100.0	212	9	US-09-991-073-387
8	1102	100.0	212	9	US-09-990-442-387
9	1102	100.0	212	9	US-09-991-163-387
10	1102	100.0	212	9	US-09-993-604-387
11	1102	100.0	212	9	US-09-990-456-387
12	1102	100.0	212	9	US-09-989-721-387
13	1102	100.0	212	9	US-09-992-598-387
14	1102	100.0	212	9	US-09-989-293A-387
15	1102	100.0	212	9	US-09-989-735-387

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20 1102 100.0 212 9 US-09-993-687-387
21 1102 100.0 212 10 US-09-989-734-387
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44 1102 100.0 212 10 US-09-997-349-387
45 1102 100.0 212 10 US-09-997-440-387

ALIGNMENTS

RESULT 1

US-09-989-722-387
; Sequence 387, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

1 PRIOR APPLICATION NUMBER: 60/065186
2 PRIOR FILING DATE: 1997-11-12
3 PRIOR APPLICATION NUMBER: 60/065311
4 PRIOR FILING DATE: 1997-11-13
5 PRIOR APPLICATION NUMBER: 60/066770
6 PRIOR FILING DATE: 1997-11-24
7 PRIOR APPLICATION NUMBER: 60/075945
8 PRIOR FILING DATE: 1998-02-25
9 PRIOR APPLICATION NUMBER: 60/078910
10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/083322
12 PRIOR FILING DATE: 1998-04-28
13 PRIOR APPLICATION NUMBER: 60/084600
14 PRIOR FILING DATE: 1998-05-07
15 PRIOR APPLICATION NUMBER: 60/087106
16 PRIOR FILING DATE: 1998-05-28
17 PRIOR APPLICATION NUMBER: 60/087607
18 PRIOR FILING DATE: 1998-06-02
19 PRIOR APPLICATION NUMBER: 60/087609
20 PRIOR FILING DATE: 1998-06-02
21 PRIOR APPLICATION NUMBER: 60/087759
22 PRIOR FILING DATE: 1998-06-02
23 PRIOR APPLICATION NUMBER: 60/087827
24 PRIOR FILING DATE: 1998-06-03
25 PRIOR APPLICATION NUMBER: 60/088021
26 PRIOR FILING DATE: 1998-06-04
27 PRIOR APPLICATION NUMBER: 60/088025
28 PRIOR FILING DATE: 1998-06-04
29 PRIOR APPLICATION NUMBER: 60/088026
30 PRIOR FILING DATE: 1998-06-04
31 PRIOR APPLICATION NUMBER: 60/088028
32 PRIOR FILING DATE: 1998-06-04
33 PRIOR APPLICATION NUMBER: 60/088029
34 PRIOR FILING DATE: 1998-06-04
35 PRIOR APPLICATION NUMBER: 60/088030
36 PRIOR FILING DATE: 1998-06-04
37 PRIOR APPLICATION NUMBER: 60/088033
38 PRIOR FILING DATE: 1998-06-04
39 PRIOR APPLICATION NUMBER: 60/088326
40 PRIOR FILING DATE: 1998-06-04
41 PRIOR APPLICATION NUMBER: 60/088167
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43 PRIOR APPLICATION NUMBER: 60/088202
44 PRIOR FILING DATE: 1998-06-05
45 PRIOR APPLICATION NUMBER: 60/088212
46 PRIOR FILING DATE: 1998-06-05
47 PRIOR APPLICATION NUMBER: 60/088217
48 PRIOR FILING DATE: 1998-06-05
49 PRIOR APPLICATION NUMBER: 60/088655
50 PRIOR FILING DATE: 1998-06-09
51 PRIOR APPLICATION NUMBER: 60/088734
52 PRIOR FILING DATE: 1998-06-10
53 PRIOR APPLICATION NUMBER: 60/088738
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58 PRIOR FILING DATE: 1998-06-10
59 PRIOR APPLICATION NUMBER: 60/088824
60 PRIOR FILING DATE: 1998-06-10
61 PRIOR APPLICATION NUMBER: 60/088826
62 PRIOR FILING DATE: 1998-06-10
63 PRIOR APPLICATION NUMBER: 60/088858
64 PRIOR FILING DATE: 1998-06-11
65 PRIOR APPLICATION NUMBER: 60/088861
66 PRIOR FILING DATE: 1998-06-11
67 PRIOR APPLICATION NUMBER: 60/088876
68 PRIOR FILING DATE: 1998-06-11
69 PRIOR APPLICATION NUMBER: 60/089105
70 PRIOR FILING DATE: 1998-06-12
71 PRIOR APPLICATION NUMBER: 60/089440
72 PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VPREATEISHVLLCNVTQVSFWFVVTDPSSKHHTLPAVEVQSAIRKMKRINNAFFLND 120
QY 121 QTLFLKIPSTLAPPMDPSVPIIIFGVIIFCIIIVAIALLILSGIWQRKKNKPSSEVD 180
Db 121 QTLFLKIPSTLAPPMDPSVPIIIFGVIIFCIIIVAIALLILSGIWQRKKNKPSSEVD 180
QY 181 DAEDKCNMTIENGIESDPLDMKGGILMMPS 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212

RESULT 2
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; Sequence 387, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VPKREATEISHVLLCNVTQSVFVWVTPDSKNTLPAVEVQSAIRKNNKRNINNAFLND 120
Qy 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALILSGIWRKRNKKEPSEVD 180
Db 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALILSGIWRKRNKKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212
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RESULT 3
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; Sequence 387, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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1998-07-07	PRIOR FILING DATE: 1998-07-07
60/092182	PRIOR APPLICATION NUMBER: 60/092182
1998-07-09	PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;

Best Local Similarity 100.0%; Pred. No. 3.5e-113;

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Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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db 1 MLWLLFEELYTAIHAELCOPGAENAFKVRLSIBRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

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121 OTLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVATAILLSGIWORRRKKEPSEVD 180

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181 DAEKCNMTTENGPSDPI.DWKGGT.MWPS 212

RESULT 4

US-09-989-727-387

; Sequence 387, Application US/09989727

; Patent No. US20020072497A1

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleo

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Corbittson, Mark

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Andrew

APPLICANT: GODDARD, AUDREY
APPLICANT: GODOWSKI, PAUL

APPLICANT: GRIMALDI, J. Chri

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas

; APPLICANT: Roy, Margaret A

1	APPLICANT:	Stewart, Timothy A.
2	APPLICANT:	Tumas, Daniel
3	APPLICANT:	Watarabe, Colin K.
4	APPLICANT:	Williams, P. Mickey
5	APPLICANT:	Wood, William I.
6	APPLICANT:	Zhang, Zemin
7	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
8	TITLE OF INVENTION:	Acids Encoding the Same
9	FILE REFERENCE:	P2730PIC65
10	CURRENT APPLICATION NUMBER:	US/09/989,727
11	CURRENT FILING DATE:	2001-11-19
12	PRIOR APPLICATION NUMBER:	60/049787
13	PRIOR FILING DATE:	1997-06-16
14	PRIOR APPLICATION NUMBER:	60/062250
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16	PRIOR APPLICATION NUMBER:	60/065186
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3.5e-113;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 VNRREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSAIRMKRINNAFFLND 120
 DB 61 VNRREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSAIRMKRINNAFFLND 120
 QY 121 QLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAILLISGIWRRRKNKPSBYD 180
 DB 121 QLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAILLISGIWRRRKNKPSBYD 180
 QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
 DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212

RESULT 5
 US-09-989-731-387
 ; Sequence 387, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Iuc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMLFLVTAIAHELCPGAENAFKVRISRTALGDKAYAWTNEEYLPKAMVAFSMRK 60
Db 1 MLMLFLVTAIAHELCPGAENAFKVRISRTALGDKAYAWTNEEYLPKAMVAFSMRK 60

QY 61 VPKREATEISHVLLCNVTQVSFVFVVDPSKXHTLPVEVQSAIRMNKNRINNAPFLND 120
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QY 121 QTLBPLKIPSTLAPPDPSVPIIIIFGVIFCIIVAIALLILSGIWRORRKNKEPSEVD 180
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QY 181 DAEDKCNMTIENGIPSDPLDMKGGLMMP 212
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RESULT 6
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; Sequence 387, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
; CURRENT APPLICATION NUMBER: US/09/989,732
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLPFLVTAHAEIQCPCGAENAFKVLRIKRTALGDKAYADTNEEYLFKAWVAFSMRK 60
Db 1 MLWLLPFLVTAHAEIQCPCGAENAFKVLRIKRTALGDKAYADTNEEYLFKAWVAFSMRK 60
Qy 61 VPNEATEISHVLLCNVTQVSFWFVVTDPDSKNTLPAVEVQSAIRNMKRRINNAFLND 120
Db 61 VPNEATEISHVLLCNVTQVSFWFVVTDPDSKNTLPAVEVQSAIRNMKRRINNAFLND 120
Qy 121 QTLBFLKIPSTLAPPMDSVPIMIIIFGVIFCIIVAIALLILSGIWORRRKKEPSEVD 180
Db 121 QTLBFLKIPSTLAPPMDSVPIMIIIFGVIFCIIVAIALLILSGIWORRRKKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212

RESULT 7
US-09-991-073-387
; Sequence 387, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLFPLVTAHAELCQGAENAFKVRLSIRLTALGDKYAYNDTWEYLFKANVAFSRYK 60
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QY 61 VFNREATEISHVLLCNVQSFVFWVTPDSKNHTLPAYVQSARIMNKNRINNAFFLND 120
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QY 181 DAEDKCNMTTENGIPSPDLNKGGLMPPS 212
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Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Fong, Sherman
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APPLICANT: Geritsen, Mary E.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990.442
CURRENT FILING DATE: 2001-11-14
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;

Best Local Similarity 100.0%; Pred. No. 3.5e-113; Mismatches 0; Indels 0; Gaps 0;

Matches 212; Conservative 0;

QY 1 MLWLLFFLVTAHAEBCQFGAENAFKVLRSIRTAIGDKAYAWDTNNEEYLFKAWVAFSMRX 60
 DB 1 MLWLLFFLVTAHAEBCQFGAENAFKVLRSIRTAIGDKAYAWDTNNEEYLFKAWVAFSMRX 60
 QY 61 VFNREATEISHVLLCNVTORUSFWPVVTDPSKNHTLPAVEVOSAIRMKNKRNINNAFFLND 120
 DB 61 VFNREATEISHVLLCNVTORUSFWPVVTDPSKNHTLPAVEVOSAIRMKNKRNINNAFFLND 120
 QY 121 QTLBFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLISGIWRRRKNKEPSEVD 180
 DB 121 QTLBFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLISGIWRRRKNKEPSEVD 180
 QY 181 DAEDKCNMNTIENGIPSDPLDMKGGILMPS 212
 DB 181 DAEDKCNMNTIENGIPSDPLDMKGGILMPS 212

RESULT 9

US-09-991-163-387

Sequence 387, Application US/09991163

Patent No. US20020132253A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

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APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730PIC17

CURRENT APPLICATION NUMBER: US/09/991,163

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/088029


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7 PRIOR FILING DATE: 1998-07-07
7 PRIOR APPLICATION NUMBER: 60/092182
7 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 QTLEPLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVALLISGIWQRKKRKPSEVD 180

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Db 121 QTLEPLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVALLISGIWQRKKRKPSEVD 180
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RESULT 10
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; Sequence 387, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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61 PRIOR APPLICATION NUMBER: 60/091633
62 PRIOR FILING DATE: 1998-07-02
63 PRIOR APPLICATION NUMBER: 60/091978
64 PRIOR FILING DATE: 1998-07-07
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66 PRIOR FILING DATE: 1998-07-07
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68 PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 1102; DE 9; Length 212;
Best Local Similarity 100.08; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
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Sequence 387, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC55
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; Sequence 387, Application US/09992598
; Patent No. US20020150384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Sotstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Fong, Sherman
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; APPLICANT: Geritsen, Mary E.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; Patent No. US20020177164A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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128 PRIOR FILING DATE: 1998-06-25
129 PRIOR APPLICATION NUMBER: 60/090694
130 PRIOR FILING DATE: 1998-06-25
131 PRIOR APPLICATION NUMBER: 60/090695
132 PRIOR FILING DATE: 1998-06-25
133 PRIOR APPLICATION NUMBER: 60/090696
134 PRIOR FILING DATE: 1998-06-25
135 PRIOR APPLICATION NUMBER: 60/090862
136 PRIOR FILING DATE: 1998-06-26
137 PRIOR APPLICATION NUMBER: 60/090863
138 PRIOR FILING DATE: 1998-06-26
139 PRIOR APPLICATION NUMBER: 60/091360
140 PRIOR FILING DATE: 1998-07-01
141 PRIOR APPLICATION NUMBER: 60/091478
142 PRIOR FILING DATE: 1998-07-02
143 PRIOR APPLICATION NUMBER: 60/091544
144 PRIOR FILING DATE: 1998-07-01
145 PRIOR APPLICATION NUMBER: 60/091519
146 PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMLLFLVTAIHAELCOPGAEAFKVRSLRTALGDKAYADNTEYLFKAMVAFSMRK 60
Db 1 MMLLFLVTAIHAELCOPGAEAFKVRSLRTALGDKAYADNTEYLFKAMVAFSMRK 60

Qy 61 VPNEATEISHVLLCNVTQVSFVFVVDTSKXHTLPAVEVQSAIRNMKNRINNAPFLND 120
Db 61 VPNEATEISHVLLCNVTQVSFVFVVDTSKXHTLPAVEVQSAIRNMKNRINNAPFLND 120

Qy 121 QTLEFLKIPSTLAPMDPSVPINIIIFGVIFCIIIVAIALLISGIMORRKNKBPSEVD 180
Db 121 QTLEFLKIPSTLAPMDPSVPINIIIFGVIFCIIIVAIALLISGIMORRKNKBPSEVD 180

Qy 181 DAEDKCNMTIENGISDPLDKGGILMWPSS 212
Db 181 DAEDKCNMTIENGISDPLDKGGILMWPSS 212

RESULT 15
US-09-989-735-387
Sequence 387, Application US/09989735
Publication No. US20020192299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
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;; PRIOR APPLICATION NUMBER: 60/091544
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3 5e-113; Indels 0; Gaps 0;
Matches 212; Conservative 0; Mismatches 0;

Qy 1 MLWLLFFLVTAHAELOCPGAENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAHAELOCPGAENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy 61 VPNEATEISHVLLCNVTQSVFVVDPSKNHTLPAVEVQSAIRNNKRNINNAFFLND 120
Db 61 VPNEATEISHVLLCNVTQSVFVVDPSKNHTLPAVEVQSAIRNNKRNINNAFFLND 120

Qy 121 QTLFELKIPSTLAPPMPSVPINIIIFGVIFCIIVAIALLILSGIWORRRKNKEPSEVD 180
Db 121 QTLFELKIPSTLAPPMPSVPINIIIFGVIFCIIVAIALLILSGIWORRRKNKEPSEVD 180

Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212

Search completed: April 1, 2004, 16:33:44
Job time : 43 secs

R; Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
 J. Immunol. 143, 3390-3395, 1989
 A:Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CA
 A:Reference number: A37009; MUID:90038499; PMID:2681416
 A:Accession: A37009
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-363 <ZHO>
 A:Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333
 C:Superfamily: human cell adhesion protein CD44
 C:Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 8.0%; Score 88; DB 2; Length 363;
 Best Local Similarity 21.6%; Pred. No. 1.9;
 Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPMDPSVPTWIIIFGVICIIIVALLILSGIWQRRR-----PLDMKGGI 207
 Db 256 VTTTSGPMRRPQIPWLI---LASLLALILAVCIANRRRCQKQKLVINGNGTV 312
 Qy 172 KNKPEVDADKCNMTIENGIPSD-----PLDMKGGI 207
 Db 313 EDRKPSLNGEASKQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 363

RESULT 10
 A34424
 CD44 membrane glycoprotein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
 C:Accession: A34424; A34907
 R:Nottingham, C.; Rees, G.; St. John, T.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
 A:Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
 A:Reference number: A34424; MUID:90046829; PMID:2682651
 A:Accession: A34424
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-365 <NOT>
 A:Cross-references: GB:M27130; NID:g195530; PIDN:AAA37407.1; PID:g309161
 R:Wolfe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
 J. Biol. Chem. 265, 341-347, 1990
 A:Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen
 A:Reference number: A34907; MUID:90094420; PMID:2403559
 A:Accession: A34907
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 8-195, 'G', 197-365 <WOL>
 A:Cross-references: GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g200335
 C:Superfamily: human cell adhesion protein CD44
 C:Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 8.0%; Score 88; DB 2; Length 365;
 Best Local Similarity 21.6%; Pred. No. 1.9;
 Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPMDPSVPTWIIIFGVICIIIVALLILSGIWQRRR-----PLDMKGGI 207
 Db 258 VTTTSGPMRRPQIPWLI---LASLLALILAVCIANRRRCQKQKLVINGNGTV 314
 Qy 172 KNKPEVDADKCNMTIENGIPSD-----PLDMKGGI 207
 Db 315 EDRKPSLNGEASKQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 365

RESULT 11
 A35616
 T-cell surface glycoprotein CD44 - hamster
 C:Species: Cricetinae Gen. sp. (hamster)
 C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
 C:Accession: A35616
 R:Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
 Cell 61, 1303-1313, 1990

A:Title: CD44 is the principal cell surface receptor for hyaluronate.
 A:Reference number: A35616; MUID:90304889; PMID:1694723
 A:Accession: A35616
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-362 <ARU>
 C:Superfamily: human cell adhesion protein CD44
 C:Keywords: cell adhesion; glycoprotein; transmembrane protein

Query Match 7.8%; Score 86; DB 2; Length 362;
 Best Local Similarity 22.0%; Pred. No. 2.9;
 Matches 24; Conservative 22; Mismatches 29; Indels 34; Gaps 3;

Qy 130 STLAPMDPSVPTWIIIFGVICIIIVALLILSGIWQRRR-----KN 173
 Db 257 TTSRPGKRPQIPWLI---VLASLLALILAVCIANRRRCQKQKLVINGNGKVED 313
 Qy 174 KNKPEVDADKCNMTIENGIPSD-----PLDMKGGI 207
 Db 314 RKPSELNGEASKQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 362

RESULT 12
 B38745
 Cell adhesion molecule CD44 precursor, long form (meta-1) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 05-Nov-1999
 C:Accession: B38745; A38745
 R:Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, S.
 Cell 65, 13-24, 1991
 A:Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcino
 A:Reference number: A38745; MUID:91191552; PMID:1707342
 A:Accession: B38745
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-503 <GUE>
 A:Cross-references: GB:M61874; NID:g576534; PIDN:AAA53534.1; PID:g576535
 A:Accession: A38745
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-223, 386-503 <GU2>
 A:Cross-references: GB:M61875
 C:Keywords: cell adhesion

Query Match 7.8%; Score 86; DB 2; Length 503;
 Best Local Similarity 20.7%; Pred. No. 4.3;
 Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPMDPSVPTWIIIFGVICIIIVALLILSGIWQRRR----- 171
 Db 396 VTTTSGPARPQIPWLI---LASLLALILAVCIANRRRCQKQKLVINGNGTV 452
 Qy 172 KNKPEVDADKCNMTIENGIPSD-----PLDMKGGI 207
 Db 453 EDRKPSLNGEASKQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 503

RESULT 13
 T47482
 receptor-like protein kinase - Arabidopsis thaliana
 N:Alternate names: protein Fl8N11.180
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
 C:Accession: T47482
 R:Jordan, N.; Bangert, S.; Wiedemann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
 submitted to the Protein Sequence Database, February 2000
 A:Reference number: Z24467
 A:Accession: T47482
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-667 <JOR>
 A:Cross-references: EMBL:AL132953
 A:Experimental source: cultivar Columbia; BAC clone Fl8N11

C:Genetics:
 A:Map position: 3
 A:Note: F18N11.180
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 7.8%; Score 85.5; DB 2; Length 667;
 Best Local Similarity 21.6%; Pred. No. 6.6;
 Matches 37; Conservative 23; Mismatches 64; Indels 47; Gaps 6;

QY 81 YSFWVVTDSKNHTLPAVEVQSAR-----MKNKRNNAFF 117
 DB 192 VQWIDYDGLNVTLPAPIHQKPNRLISRDINLSIFQDKMVGSGNGRLTNCQYI 251
 QY 118 LN-----DOTLEFLKIPSTLAP-----PMDSVPWIIIFGVIFCIIVAIALAL 161
 DB 252 LGSFSKSKFMQSLDKLPQAPIPNEQAPVREKXKLLPGLGLV--ILLVIPVLM 309
 QY 162 ILGSI-WQRRKKNKEPSVDAAE-----DKCNMTIENGIPSDPLDMKGG 206
 DB 310 VLGGVYRKRKYAEVXESWEKEYGPHRYGKSLYKATNGFVKDALVGKGG 360

RESULT 14
 E81924
 probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
 C:Species: Neisseria meningitidis
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: E81924
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: E81924
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-468 <PAR>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:G7379424; PIDN:CAB84080.1; PID:G737951
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA0797
 C:Keywords: phosphotransferase

Query Match 7.7%; Score 84.5; DB 2; Length 468;
 Best Local Similarity 23.7%; Pred. No. 5.4;
 Matches 47; Conservative 29; Mismatches 81; Indels 41; Gaps 9;

QY 21 AENAFKVRLSIRTL-----GDKAYADTNEEYLFKAMVAFSMKVPNREATEI 69
 DB 34 AENQFNQRTIETTLGSIISAFRAGD-AGAREILTEWK-DSPVSSGVTVIQDDEKQI 91
 QY 70 SHVLLCNVTQVSVFWVVDPSKXHTLPAVEVQSAIRMKNRINN--AFLIND-QLLEFL 126
 DB 92 LERYIDSYTIERARLFAAGHPHN-----LVHIYDRFGEELYLFTKDWDXLQAR 141
 QY 127 KIPSTLAPMPSVPIW-----IIFGVIFCIIV--VAIALILSGIWKOR-----RR 171
 DB 142 RLSPSLPIPLGPIPIWHHEILLSFIIIVGLLMAYILAGNAKEIRILGNDRVANGEL 201
 QY 172 KNKEPSVDDAEDKCNM 189
 DB 202 ETRISQQVDRDDELHL 219

RESULT 15
 JG0022
 flagellar basal-body M-ring protein flippin - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 21-Jul-2000
 C:Accession: JG0022; A42365; B69624; S14494
 R:Zuberi, A.R.; Ying, C.; Bischoff, D.S.; Ordal, G.W.
 Gene 101, 23-31, 1991
 A:Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus

A:Reference number: JG0019; MUID:91285431; PMID:1905667
 A:Accession: JG0022
 A:Molecule type: DNA
 A:Residues: 1-536 <ZUB>
 A:Cross-references: GB:M54965
 R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
 J. Bacteriol. 173, 3573-3579, 1991
 A:Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flag
 A:Reference number: A42365; MUID:91258343; PMID:1828465
 A:Accession: A42365
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 355-536 <ALB>
 A:Cross-references: GB:M72718; EMBL:X56049; NID:G39904; PIDN:CAA39520.1; PID:G3979709
 R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Leuber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
 keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshihida,
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: B69624
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-536 <KUN>
 A:Cross-references: GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CAB13494.1; PID:el185212
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: flipp

Query Match 7.7%; Score 84.5; DB 2; Length 536;
 Best Local Similarity 19.9%; Pred. No. 6.3;
 Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;

QY 9 VTAIHAELCQGAENAFKVRLSIRTLGDKAYADTNEEYLFKAMVAFSMKVPNREATE 68
 DB 352 VRIHKEI-----AESPIKVR-----DLGIQWVEPPDAKNTASLSTERQDD 393
 QY 69 ISHVLLCNVTQVSVFWVVDPSKXHTLPAVEVQSAIRMKNRINNNAFFINDOTLFLKI 128
 DB 394 IQKIL--STVVRTS---LQKDETQNLSDADINNKIVVSVQVFDGKVNLDNTTE--- 444
 QY 129 PSTLAPMPSVPIW--IIFGVIFCIIVAIALLILSGIWKORRKNKEPSVDDADKCE 187
 DB 445 -----SSGIFLWAYIVGGVLIAAIIVLIIMLI-----KKGAQSDSPFEYEY--- 487
 QY 188 NMTIENGIPSDPLDM 203
 DB 488 -----VQEPINL 495

Search completed: April 1, 2004, 16:28:26
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:23:18 ; Search time 18 Seconds
(without alignments)
613.271 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102

Sequence: 1 MLWLLFFLVTAHAEICQPG.....ENGIPSDPLDMKGILMPS 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.5	8.4	1153	1	NOS LYMST
2	91	8.3	623	1	SVR_SULTO
3	90	8.2	799	1	CAD8_MOUSE
4	90	8.2	799	1	CAD8_MOUSE
5	89.5	8.1	1025	1	ITAB_HUMAN
6	89	8.1	799	1	CAD8_HUMAN
7	88	8.0	778	1	CD44_MOUSE
8	87	7.9	362	1	CD44_CRIGR
9	86	7.8	431	1	CD44_MSAU
10	86	7.8	503	1	CAD4_RAT
11	84.5	7.7	536	1	FLIF_BACSU
12	83.5	7.6	1337	1	PTPJ_HUMAN
13	82.5	7.5	1044	1	ITAB_CHICK
14	82	7.4	1189	1	ITAB_HUMAN
15	81.5	7.4	363	1	LEU3_PHOLL
16	81.5	7.4	1048	1	ITAB_HUMAN
17	81	7.4	1179	1	ITAB_MOUSE
18	80.5	7.3	1034	1	ITAB_CHICK
19	80	7.3	234	1	VGP8_EBV
20	79.5	7.2	393	1	IL1S_CERAE
21	79.5	7.2	1044	1	ITAB_MOUSE
22	79	7.2	437	1	YC44_PORPU
23	79	7.2	611	1	REB3_MOUSE
24	79	7.2	1033	1	ITAB_MOUSE
25	79	7.2	2029	1	LAR_DROME
26	78	7.1	343	1	MRGF_RAT
27	78	7.1	732	1	CADL_CHICK
28	78	7.1	1022	1	ADAI1_ANGAN
29	77.5	7.0	351	1	CD44_CANFA
30	77	7.0	322	1	GPT_SULSO
31	76.5	6.9	363	1	LEU3_SALTY
32	76.5	6.9	365	1	OPSR_XENLA
33	76.5	6.9	475	1	MUC1_HYLLA

34	76	6.9	1337	1	YDM5_SCHPO	P87136 schizosacch
35	75.5	6.9	549	1	YUCE_ECOLI	P32703 escherichia
36	75.5	6.9	1255	1	MUC1_HUMAN	P15941 h mucin 1 p
37	75	6.8	343	1	MRGF_MOUSE	Q8vcj6 mus musculu
38	75	6.8	357	1	OPSR_ORYLA	P87367 oryzias lat
39	75	6.8	1007	1	GRD2_MOUSE	Q61625 mus musculu
40	75	6.8	1007	1	GRD2_RAT	Q63226 rattus norv
41	75	6.8	1428	1	ATRN_MOUSE	Q9wu60 mus musculu
42	74.5	6.8	307	1	TR41_HUMAN	P59536 homo sapien
43	74.5	6.8	307	1	TR59_HUMAN	P59550 homo sapien
44	74.5	6.8	348	1	TRNF_VIBPA	Q8mxl1 vibrio para
45	74.5	6.8	379	1	MCP_CAVPO	P70105 cavia porce

ALIGNMENTS

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RESULT 1
NOS LYMST
ID NOS LYMST STANDARD; PRT; 1153 AA.
AC O61309;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric-oxide synthase (EC 1.14.13.39) (NOS, type I) (Neuronal NOS)
DE (N-NOS) (nNOS).
GN NOS.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RC SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RP TISSUE=CNS;
RX MEDLINE=98211896; PubMed=9552167;
RA Korneev S.A., Piper M.R., Picot J., Phillips R., Korneeva E.I.,
RA O'Shea M.;
RT Molecular characterization of NOS in a mollusc: expression in a giant
RT modulatory neuron.;
RL J. Neurobiol. 35:65-76(1998).
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body (By similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + NADPH + H2O = citrulline +
CC nitric oxide + NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN (By
CC similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O61309-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O61309-2; Sequence=VSP_003584;
CC -!- TISSUE SPECIFICITY: Expressed in the central nervous system, in
CC the serotonergic cerebral giant cells. Both the long and short
CC isoforms are expressed equally in the CNS.
CC -!- SIMILARITY: belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF012531; AAC17487.1; --
CC F1R; T31080; T31080.
CC HSP; P29477; 1DD7.
CC InterPro: IPR003097; FAD_binding.
CC InterPro: IPR008254; Flav_nitox_synth.
CC InterPro: IPR001094; Flavodoxin_like.

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DR InterPro; IPR001709; FPN_cyt_redtse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 2.
DR Pfam; PF02898; NO_synthase_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Repeat;
KW Alternative splicing.
FT DOMAIN 427 610
FT METAL 82 82
FT DOMAIN 397 417
FT NP_BIND 556 587
FT NP_BIND 697 708
FT NP_BIND 836 846
FT NP_BIND 911 929
FT NP_BIND 1089 1104
FT DOMAIN 934 1010
FT VARSPLIC 276 309
FT Missing (in isoform Short).
FT /FTID=VSP_003584.
SQ SEQUENCE 1153 AA; 129085 MW; 101B7D02B66B109 CRC64;

Query Match 8.4%; Score 92.5; DB 1; Length 1153;
Best Local Similarity 21.1%; Pred.No.1.7; Indels 135; Gaps 13;
Matches 64; Conservative 28; Mismatches 135; Indels 135; Gaps 13;

QY 21 AENAFKVRISRTALGKAYAMDTNEEYLFA-MVAFSMRKVPNRE---ATEI----- 69
DB 689 AENA---TDLYAPGDHVAIPFANSPEIVDAILLVRLDTSGPSDPQVVKTEISTQLGTN 744
QY 70 ----SHVLLCVTVQSVFVWVTDPSKHTLPAVEVQSAIRMKVRI-----NNAFF--- 117
DB 745 DTRSHLPICTSRTAFLVDTTPPSQBILOVLATQASSMDKHKLQLASNAYEAKM 804
QY 118 ---LNDQTLF-----LKIPSTL----- 132
DB 805 RLDSLNTLEILDEPPLSKIPSLALLTQLPLQPRVYSSSQKXNPNVEHATIAVVRPK 864
QY 133 -----AP-----PMDSPVIMIIIFGVIFCIIV 156
DB 865 TDQGDGPVHEGVCSWLNRSPICTVVPCLRSAPHFLPEDPSLPIMIGPQ----- 916
QY 157 ATALLILSGI-----WQERRKNKPSVEVDAEDKCN-MITIENGIPSDPLDMKGGILM 209
DB 917 -----SGIAPRFSWQRL-----GEIENTWPSCENTMLSCETTIPSCNSMPSCENT 964
QY 210 MPS 212
DB 965 MPS 967

RESULT 2
SYR_SULTO
ID SYR_SULTO STANDARD; PRT; 623 AA.
AC Q971X1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
GN ARGS OR ST1258.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;

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RA Kavarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama H., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiya M., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
CC -|- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC EMBL; AP000985; BAB66299.1; -.
DR HAMAP; MF_00123; -. 1.
DR InterPro; IPR001278; Arg_tRNA-synt_1c.
DR InterPro; IPR008909; tRNA-synt_id_C.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00750; tRNA-synt_id_1.
DR Pfam; PF05746; tRNA-synt_id_C; 1.
DR PRINTS; PR01038; TRNASYNTHARG.
DR TIGRFAMs; TIGR00456; args; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 116 126 "HIGH" REGION.
SQ SEQUENCE 623 AA; 71692 MW; A24645D096B038B CRC64;

Query Match 8.3%; Score 91; DB 1; Length 623;
Best Local Similarity 22.1%; Pred.No.1.1; Indels 84; Gaps 12;
Matches 45; Conservative 31; Mismatches 44; Indels 84; Gaps 12;

QY 45 NEEYLFKAMVA-----PSMRKVPNREATEISHLVLCNVTVQSVFWFVTVTPSKNHTLPV 99
DB 82 NESEFLKLFITNFPEDGIEKIQKQPVVVEH-----TSANPIHPLHVG 125
QY 100 EVQSAI-----RMNQR-----INNAFLNDQ-----TLEFLXI--PSTLAPMDPSVP 141
DB 126 HLRNALIGDVIARMLKARGHEVNTRFYVNDAGRQVAILTLGYLLGSPN---PPRDEKID 182
QY 142 IWLIFGVIFCI--IIVAI-----ALLILSGIWQRRKNKEP 176
DB 183 QWI---GVIAITNIIIEINQLKELSSNEEYVQKISKIDELISLAG---KHREKYP 235
QY 177 -----SEVDDAEDKCNMI 190
DB 236 EIFDKLADEISKIENIEKIQNII 259

RESULT 3
CAD8_MOUSE
ID CAD8_MOUSE STANDARD; PRT; 799 AA.
AC P97291;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cadherin-8 precursor.
GN CDH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=97174321; PubMed=9022055;
 RA Korematsu K., Redies C.;
 RT "Restricted expression of cadherin-8 in segmental and functional
 RT subdivisions of the embryonic mouse brain.";
 RL Dev. Dyn. 208:178-189(1997).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC
 CC EMBL: X95600; CAA64857.1; -;
 DR HSSP: P15116; INCIJ;
 DR MGD: MGI:107434; Cdh8.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; cadherin; 5.
 DR Pfam: PF01049; Cadherin_C term; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 799 AA; 88200 MW; 0E33FEAD563C7F76 CRC64;
 Query Match 8.2%; Score 90; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 1.8;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;
 QY 13 HAEICQPGAEAFKVRISITLGDYAWDT-----NEEYLFKAWAFSMEKVPN 63
 DB 432 HTDLEFQFNADGGKITLPTLDRELVSWHNTIATEIRHSQISQVPVAKVLVDV-N 490
 QY 64 REATEIS----HVLIC-----NVTQVSFVFVVTDSKNH-----TLPVAVQSALRMNK 109
 DB 491 DNAPEFASEYEALFCEKNGKPGQVIQTVSA-MDKDDPENGHFYLLPEMWNPNFTIKK 549
 QY 110 NRINNAFFL-----NDOTLEFLKISTLA-----PKMDPSVPVWIIIFG----- 148
 DB 550 NEDNSLSILAKHNGFRKQKEVLLPIVISDSGNPPLSSTSTUIRVCGSGNDGVQSCN 609
 QY 149 -----VFICIIIVAILLISGMWRKRKNKEPSEVDADKCNMT 191
 DB 610 VEAVLPGLSMGALIAIACIILLIVLVLF--VTLRRKH-EPLIKDDEVDRENIIR 666
 QY 192 IEN 194
 ;;

DB 667 YDD 669
 RESULT 4
 CAD8_RAT
 ID CAD8_RAT STANDARD; PRT; 799 AA.
 AC O54800; O54801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDR8.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=98190518; PubMed=9521872;
 RA Kido M., Obata S., Tanihara H., Rochelle J.M., Seidin M.F.,
 RA Taketani S., Suzuki S.T.;
 RL Genomics 48:186-194(1998).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O54800-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O54800-2; Sequence=VSP_000638, VSP_000639;
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC
 CC EMBL: AB010436; BAA24452.1; -;
 DR EMBL: AB010437; BAA24453.1; -;
 DR HSSP: P15116; INCIJ.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C term.
 DR Pfam: PF00028; cadherin; 5.
 DR Pfam: PF01049; Cadherin_C term; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT VARSPLIC 514 532 IQTUSAMDKDPKNGHFL -> NISMILLNMFVYNCFLV
FT N (in isoform 2).
FT /FTID=VSP_000638.
FT VARSPLIC 533 799 Missing (in isoform 2).
FT /FTID=VSP_000639.
SQ SEQUENCE 799 AA; 88332 MW; FOLD145A80966C86 CRC64;

Query Match 8.2%; Score 90; DB 1; Length 799;
Best Local Similarity 21.4%; Pred. No. 1.8;
Matches 52; Conservative 34; Mismatches 91; Indels 56; Gaps 11;

QY 13 HAEICQCAENAFKVRISRTALGDKAYANDT-----NEBYLFKAMVAFNRKYPN 63
DB 432 HTDLERQFNADDDCKITLATPLDRELSVMHNISIAIEIRHNSQISRPVAKVLDV-N 490
QY 64 REATEIS---HVILIC-----NVTQVGFVFWVDPSKNH-----TLPAVEQSAIRNK 109
DB 491 DNAPEFASERYAFLCENGKPGQVITVSA-MKDDPKNGHFFLYSLPEWNNNFYIKK 549
QY 110 NRINNAFL-----NDQTLFLKIPSTLA-----PPMDPSVPIMIIIFG----- 148
DB 550 NEDNSLSILAKHNGENRQKQVYLLPIVSDGNPPLSLTSLTRVCGCSNDGVQSCN 609
QY 149 -----VFCHIIIVAIALLILSGHWQRKQKPSFVDDADKCNWIT 191
DB 610 VEPYVLPICLSMGALIAIACIILLVIVLWF--VTLRRHN-BPLIIKDDQDVRENIIR 666
QY 192 IEN 194
DB 667 YDD 669

RESULT 5
ITAB HUMAN STANDARD; PRT; 1025 AA.
AC P53708.
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Integrin alpha-8.
GN ITGA8.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286701; PubMed=7768999;
RA Schnapp L.M., Breuss J.M., Ramos D.M., Sheppard D., Pyriela R.;
RT "Sequence and tissue distribution of the human integrin alpha 8
RT subunit: a beta 1-associated alpha subunit expressed in smooth muscle
RT cells.";
RL J. Cell Sci. 108:537-544 (1995).
CC -!- FUNCTION: INTEGRIN ALPHA-8/BETA-1 IS A RECEPTOR FOR FIBRONECTIN
CC AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
CC DISULFIDE BOND. ALPHA-8 ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN SMOOTH MUSCLE AND
CC SMOOTH MUSCLE-LIKE CONTRACTILE CELLS.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC
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CC
CC EMBL; L36531; AAA93514.1; -

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```

DR HSSP; P06756; 1JUV2.
DR Genew; HGNC:6144; ITGA8.
DR XM; 604063.
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; P:cell adhesion receptor activity; NAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP 4.
DR Pfam; PF00357; integrin_A; 1.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Inc_alpha; 6.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Repeat; Calcium.
FT CHAIN 1 868 INTEGRIN ALPHA-8 HEAVY CHAIN (POTENTIAL).
FT CHAIN 869 1025 INTEGRIN ALPHA-8 LIGHT CHAIN (POTENTIAL).
FT DOMAIN 1 974 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 975 995 POTENTIAL..
FT DOMAIN 996 1025 CYTOPLASMIC (POTENTIAL).
FT REPEAT 15 79 FG-GAP 1.
FT REPEAT 161 160 FG-GAP 2.
FT REPEAT 226 279 FG-GAP 3.
FT REPEAT 280 345 FG-GAP 4.
FT REPEAT 346 405 FG-GAP 5.
FT REPEAT 409 463 FG-GAP 6.
FT CA_BIND 291 299 FG-GAP 7.
FT CA_BIND 357 365 POTENTIAL.
FT SITE 421 429 POTENTIAL.
FT SITE 417 419 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 58 68 BY SIMILARITY.
FT DISULFID 112 133 BY SIMILARITY.
FT DISULFID 149 162 BY SIMILARITY.
FT DISULFID 469 480 BY SIMILARITY.
FT DISULFID 486 542 BY SIMILARITY.
FT DISULFID 603 609 BY SIMILARITY.
FT DISULFID 675 688 BY SIMILARITY.
FT DISULFID 829 886 INTERCHAIN (BY SIMILARITY).
FT DISULFID 891 896 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 699 699 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 715 715 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 858 858 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 885 885 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 967 967 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1025 AA; 113612 MW; 58BB6B2C00CF7B93 CRC64;

Query Match 8.1%; Score 89.5; DB 1; Length 1025;
Best Local Similarity 20.2%; Pred. No. 2.8;
Matches 34; Conservative 35; Mismatches 40; Indels 59; Gaps 8;

QY 20 GAENAFKVRISRTALGDKAYAMDTNEEYLFKAMVAFNRKQKPSFVDDADKCNWITQ 79
DB 903 GGESAV---LKVRSLWAHTFLQKNDPFYALASVSVKMPYTD----- 945
QY 80 RVSMFVVDPSKNHTLP--AVEVQSAIRMNKRINNAFLNDQTLFLKIPSTLAPPMD 137
DB 946 -----QPAK---LPEGSIATKTSV-----IWAT--PNVS 969
QY 138 PSVPFIIVFGVFCIIIVAIALLIL--SGIWRRRKRNKPSFVDDADK 183
DB 970 FSIPLWIIAILLGLVLAITLALWKCQGFDRARPQEQ--DMTDRE 1015

```

RESULT 6
 ID CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P5286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Teujimoto G., Kitajima M., Katori M.;
 RT "Identification of three human type-II classic cadherins and frequent heterophilic interactions between different subclasses of type-II classic cadherins.";
 RT Biochem. J. 349:159-167(2000).
 RL [2]
 RN SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heimark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of cadherin extracellular domain and provides further evidence for two structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain nerve cell lines, such as retinoblasts, glioma cells and neuroblasts.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC
 CC EMBL; AB035305; BAB87419.1; -;
 CC EMBL; L34060; AAA35628.1; ALT_INIT.
 CC HSSP; P15116; INCIJ.
 CC Genew; HGNC:1767; CDH8.
 CC MIN; 603008;
 CC GO; GO:0007155; P:cell adhesion; TAS.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR002033; Cadherin_C_term.
 CC Pfam; PF00028; cadherin; 5.
 CC Pfam; PF01049; Cadherin_C_term; 1.
 CC PRINTS; PR0205; CADHERIN.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal.

FT	SIGNAL	1	29	POTENTIAL.
FT	PROPEP	30	61	POTENTIAL.
FT	CHAIN	62	799	CADHERIN-8.
FT	DOMAIN	62	621	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	622	642	POTENTIAL.
FT	DOMAIN	643	799	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	62	167	CADHERIN 1.
FT	DOMAIN	168	276	CADHERIN 2.
FT	DOMAIN	277	331	CADHERIN 3.
FT	DOMAIN	392	494	CADHERIN 4.
FT	DOMAIN	495	616	CADHERIN 5.
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	473	473	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	544	544	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	355	355	V -> D (IN REF. 2 AND 3).
FT	CONFLICT	647	647	H -> HQ (IN REF. 2 AND 3).
SQ	SEQUENCE	799 AA;	88253 MW;	9B119B86039CGA0A CRC64;

Query Match 8.1%; Score 89; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 2.3;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

OY	13	HAEICOPGAENAFKVLRLSIRLTALGDKAYAWDT-----NBEYLFKAMVAFSMEKVPN	63
DB	432	HTDLEQFNINADDGKITLATPLDRLSVWHNITITATIRNHSQISRPVALKVLVDV-N	490
OY	64	REATEIS-----HYLLC-----NVTQVSPFWVVDPSKNH-----TLPAVEVQSARIMNK	109
DB	491	DNAPEPASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLPVMVNNPFTTK	549
OY	110	NRINNAFFL-----NDQTLFLFKIPSTLA-----PPMDSPVPIIIFG-----	148
DB	550	NEDNSLSILAKNGFRQKQEVYLLPIIISDSGNPLSTSTLTIRVCGSNQGVVQSCN	609
OY	149	-----VIFCIIVAIALLISGLWQRKKNKEPSEVDDAEDCKENMIT	191
DB	610	VEAYVLPICLSMGALITAILLIVIVLFP-VTLRRHN-EPLIKDDDEDVRENIIR	666
OY	192	IEN 194	
DB	667	YDD 669	

RESULT 7
 CD44_MOUSE STANDARD; PRT; 778 AA.
 AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
 AC Q62409; Q64296; Q99J14; Q9QX8;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
 DE Extracellular matrix receptor-III (ECMR-III) (GP90 lymphocyte
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
 DE (LY-24).
 DE CD44.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
 RC STRAIN=DNA/2; TISSUE=Lung;
 RX MEDLINE=93107170; PubMed=1469058;
 RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;
 RT "Molecular isoforms of murine CD44 and evidence that the membrane proximal domain is not critical for hyaluronate recognition.";
 RL J. Cell Biol. 119:1711-1719(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90038499; PubMed=2681416;
 RA Zhou D.F.H., Ding J.P., Pickler L.J., Bargatzke R.F., Butcher E.C.,
 RA Goeddel D.V.,
 RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the
 RT human H-CAM (Hermes) lymphocyte homing receptor.";
 RL J. Immunol. 143:3390-3395 (1989).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 13).
 RX MEDLINE=90046829; PubMed=2682651;
 RA Nottenburg C., Rees G., St John T.,
 RA "Isolation of mouse CD44 cDNA: structural features are distinct from
 RT the primate CDNA".
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525 (1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 11).
 RX MEDLINE=20318634; PubMed=10859330;
 RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guentert U.,
 RA "Abrogation of experimental colitis correlates with increased
 RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7)".
 RL J. Exp. Med. 191:2053-2064 (2000).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 13).
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanny J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 13).
 RX STRAIN=C57BL/6J; TISSUE=Embryo;
 RL MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaudo I., Osato N., Saio N., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Iagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Leshard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Iton M., Kigawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [7]
 RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
 RX MEDLINE=90094420; PubMed=2403559;
 RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D.,
 RA August J.T.,
 RA "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell
 RT surface antigen and proteoglycan core/link proteins.";
 RL J. Biol. Chem. 265:341-347 (1990).
 RN [8]
 RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
 RX STRAIN=GR;
 RA MEDLINE=93219085; PubMed=8464707;
 RA Toelg C., Hofmann M., Herrlich P., Ponta H.,
 RA "Splicing choice from ten variant exons establishes CD44
 RT variability".
 RL Nucleic Acids Res. 21:1225-1229 (1993).
 RN [9]
 RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).
 RX STRAIN=BALB/C;
 RA MEDLINE=93286043; PubMed=8509359;
 RA Sreaton G.R., Bell M.V., Bell J.I., Jackson D.G.,
 RA "The identification of a new alternative exon with highly restricted
 RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
 RT homing receptor. Comparison of all 10 variable exons between mouse,
 RT human, and rat.";
 RL J. Biol. Chem. 268:12235-12238 (1993).
 RN [10]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).
 RX STRAIN=Swiss Webster;
 RA MEDLINE=96355396; PubMed=8702806;
 RA Yu Q., Toole B.P.,
 RA "A new alternatively spliced exon between v9 and v10 provides a
 RT molecular basis for synthesis of soluble CD44.";
 RL J. Biol. Chem. 271:20603-20607 (1996).
 CC -1- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
 CC mucosal high endothelial venule and to types I and VI collagen.
 CC Probably involved in matrix adhesion, lymphocyte activation and
 CC lymph node homing.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=13;
 CC Name=1;
 CC IsoId=P15379-14; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P15379-7; Sequence=VSP_007329;
 CC Name=3;
 CC IsoId=P15379-8; Sequence=VSP_007330;
 CC Name=4; Synonyms=M2;
 CC IsoId=P15379-4; Sequence=VSP_007331;
 CC Name=5;
 CC IsoId=P15379-9; Sequence=VSP_007332;
 CC Name=6; Synonyms=M3;
 CC IsoId=P15379-5; Sequence=VSP_005326;
 CC Name=7; Synonyms=M4;
 CC IsoId=P15379-6; Sequence=VSP_005327;
 CC Name=8;
 CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;
 CC Name=9;
 CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;
 CC Name=10;
 CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;
 CC Name=11;
 CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;
 CC Name=12; Synonyms=M1;
 CC IsoId=P15379-3; Sequence=VSP_005328;
 CC Name=13; Synonyms=M0;
 CC IsoId=P15379-2; Sequence=VSP_005329;
 CC -1- PTM: N-glycosylated (By similarity).
 CC -1- PTM: O-glycosylated; contains chondroitin sulfate glycans which
 CC can be more or less sulfated (By similarity).

CC CC -!- PTM: Phosphorylated; activation of PKC results in the
 CC CC dephosphorylation of Ser-742 (constitutive phosphorylation site),
 CC CC and the phosphorylation of Ser-708 (By similarity).
 CC CC -!- POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and
 CC CC PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-
 CC CC 24.1).
 CC CC -!- SIMILARITY: Contains 1 link domain.
 CC CC
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 CC CC
 CC CC EMBL; X65084; CAA46883.1; -
 CC CC EMBL; X65083; CAA46882.1; -
 CC CC EMBL; X66082; CAA46881.1; -
 CC CC EMBL; X66081; CAA46880.1; -
 CC CC EMBL; M30655; AAA39922.1; -
 CC CC EMBL; M27129; AAA37405.1; -
 CC CC EMBL; M27130; AAA37407.1; -
 CC CC EMBL; AJ251594; CAB61888.1; -
 CC CC EMBL; BC005676; AH05676.1; -
 CC CC EMBL; AK045226; BAC32269.1; -
 CC CC EMBL; J05163; AAA39923.1; -
 CC CC EMBL; X69724; CAA49380.1; -
 CC CC EMBL; L13611; AAA37145.1; -
 CC CC
 CC CC Query Match 8.0%; Score 88; DB 1; Length 778;
 CC CC Best Local Similarity 21.6%; Pred. No. 2.7;
 CC CC Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;
 CC CC
 CC CC QY 128 IPSTLAPPDPSPVPIWIIIGVFICIIIVAILLISGIWQRR- 171
 CC CC Db 671 VTTISGWRPQIPWELI---LASLALALILAVCIANVSRRCQKGLVINGNGTV 727
 CC CC
 CC CC QY 172 KNKPSVDADPKCNMTIENGIPSD-----PLDMKGGI 207
 CC CC Db 728 EDRKPSLNGEASKSQEMVHLVKNKEPSETPDQMTADETNLQVDMKIGV 778
 CC CC
 CC CC RESULT 8
 CC CC CD44_CRIGR STANDARD; PRT; 362 AA.
 CC CC ID CD44_CRIGR
 CC CC AC P20944;
 CC CC DT 01-FEB-1991 (Rel. 17, Created)
 CC CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC CC DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
 CC CC DE (extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
 CC CC DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
 CC CC GN CD44.
 CC CC OS Cricetus griseus (Chinese hamster).
 CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC CC OC Cricetulus.
 CC CC OX NCBI_TaxID=10029;
 CC CC RN [1]
 CC CC RP SEQUENCE FROM N.A.
 CC CC RX MEDLINE=90304889; PubMed=1694723;
 CC CC RA Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
 CC CC RT "CD44 is the principal cell surface receptor for hyaluronate.";
 CC CC RL Cell 61:1303-1313(1990).
 CC CC CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
 CC CC mucosal high endothelial venule and to types I and VI collagen.
 CC CC CC Probably involved in matrix adhesion, lymphocyte activation and
 CC CC lymph node homing.
 CC CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC CC CC -!- INDUCTION: By EBV.
 CC CC CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
 CC CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,

CC CC of phosphate to cytoplasmic domain serine residues.
 CC CC -!- SIMILARITY: Contains 1 link domain.
 CC CC
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 CC CC
 CC CC EMBL; M33827; AAA36967.1; -
 CC CC EMBL; A35616; A35616.
 CC CC HSP; P98056; ITSG.
 CC CC InterPro; IPR001231; CD44_antigen.
 CC CC InterPro; IPR000538; Link.
 CC CC Pfam; PF00193; Xlink; 1.
 CC CC DR PRINTS; PR00658; CD44.
 CC CC DR PRINTS; PR01265; LINKMODULE.
 CC CC DR ProDom; PD000918; Link; 1.
 CC CC DR SMART; SK00445; LINK; 1.
 CC CC DR PROSITE; PS01241; LINK; 1.
 CC CC KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
 CC CC KW Proteoglycan; Signal; Alternative splicing;
 CC CC KW Pyrrrolidone carboxylic acid.
 CC CC FT SIGNAL 1 22
 CC CC FT CHAIN 23 362
 CC CC FT DOMAIN 23 269
 CC CC FT TRANSMEM 270 290
 CC CC FT DOMAIN 291 362
 CC CC FT DOMAIN 50 121
 CC CC FT DOMAIN 152 160
 CC CC FT DOMAIN 226 269
 CC CC FT MOD_RES 23 23
 CC CC FT DISULFID 55 120
 CC CC FT DISULFID 79 99
 CC CC FT MOD_RES 292 292
 CC CC FT MOD_RES 326 326
 CC CC FT CARBOHYD 27 27
 CC CC FT CARBOHYD 59 59
 CC CC FT CARBOHYD 102 102
 CC CC FT CARBOHYD 112 112
 CC CC FT CARBOHYD 122 122
 CC CC FT CARBOHYD 174 174
 CC CC FT CARBOHYD 256 256
 CC CC SQ SEQUENCE 362 AA; 39775 MW; E89EB434E9EEC948 CRC64;
 CC CC
 CC CC Query Match 7.9%; Score 87; DB 1; Length 362;
 CC CC Best Local Similarity 23.9%; Pred. No. 1.4;
 CC CC Matches 26; Conservative 20; Mismatches 29; Indels 34; Gaps 3;
 CC CC
 CC CC QY 130 STLAPPDPSPVPIWIIIGVFICIIIVAILLISGIWQRR- 173
 CC CC Db 257 STSRFGKPRVPEWLI---VLASLALALILAVCIANVSRRCQKGLVINGNGKVED 313
 CC CC
 CC CC QY 174 KEPSEVDDAEDCKENMTIENGIPSD-----LDMKGGI 207
 CC CC Db 314 RKPSELNGEASKSQEMVHLVKNKEPSETPDQMTADETNLQVDMKIGV 362
 CC CC
 CC CC RESULT 9
 CC CC CD44_MESAU STANDARD; PRT; 431 AA.
 CC CC ID CD44_MESAU
 CC CC AC Q60522; Q60523;
 CC CC DT 01-NOV-1997 (Rel. 35, Created)
 CC CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC CC DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
 CC CC DE (extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
 CC CC DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)

DE (Heparan sulfate proteoglycan) (HAM1 antigen).
GN CD44.
CS Mesocricetus auratus (Golden hamster).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC Mesocricetus
CC NCBI_TaxID=10036;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP STRAIN=LVG; TISSUE=Alveolar macrophage;
RA Paulauskis J.D., Kobzik E., Gerard C., Katler M., Godleski J.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; IsoId=Q60522-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q60522-2; Sequence=VSP_005322;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-395 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-361 (By similarity).
CC -!- SIMILARITY: Contains 1 link domain.
CC
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CC -----
DR EMBL; U10880; AAC13767.1; -;
DR EMBL; U10881; AAL9316.1; -;
DR HSSP; P98066; ITSG.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PR000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 22
FT CHAIN 23 431
FT DOMAIN 23 338
FT TRANSMEM 339 359
FT DOMAIN 360 431
FT DOMAIN 501 121
FT DOMAIN 152 160
FT DOMAIN 226 338
FT MOD_RES 23 23
FT DISULFID 55 120
FT DISULFID 79 99
FT MOD_RES 361 361
FT MOD_RES 395 395
FT CARBOHYD 27 27
FT CARBOHYD 59 59
FT CARBOHYD 102 102

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 222 291 TRSGGKDGRRGGGLPKDATTSLGGYTHYPETWENGTLTPV
FT isoform 2)
FT /FTID=VSP_005322.
SQ SEQUENCE 431 AA; 46807 MW; 4300262E0C6BEA6A CRC64;
Query Match 7.8%; Score 86; DB 1; Length 431;
Best Local Similarity 22.0%; Pred. No. 2.1;
Matches 24; Conservative 22; Mismatches 29; Indels 34; Gaps 3;
QY 130 STIAPMDPSVPIIIFGVIICIIIVATLILSLGIWQRR-----KN 173
Db 326 TTSRPGKQKIPWLI---VLASLALAILAVCTAVNSRRRGQKKKLIVNSGKVED 382
QY 174 KEPEYDDADKCKENMITIENGIPSDP-----LDMKGGI 207
Db 383 RKEPELNGEASKQENVHLVNKEPFTPDQFMTADETRNLQNVDMKIGV 431
RESULT 10
CD44 RAT
ID CD44 RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
DE (LY-24).
GN CD44.
OS Rattus norvegicus (Rat).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342;
RA Gunther U., Hofmann M., Rudy W., Reber S., Zoeller M.,
RA Hausmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells";
RL Cell 65:13-24 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=2; Synonyms=Long, Meta-1;
CC IsoId=P26051-1; Sequence=Displayed;
CC Name=1; Synonyms=Short;
CC IsoId=P26051-2; Sequence=VSP_005330;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-433 (By similarity).
CC -!- SIMILARITY: Contains 1 link domain.
CC -----

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DR EMBL; M61875; AAA53532.1; -;
 DR EMBL; M61874; AAA53534.1; -;
 DR EMBL; U52179; AAA97915.1; -;
 DR EMBL; U46957; AAA92920.1; -;
 DR PIR; B38745; B38745;
 DR HSP; P98066; ITSG;
 DR InterPro; IPR001231; CD44_antigen.
 DR InterPro; IPR00538; Link.
 DR Pfam; PF00193; Link; 1.
 DR PRINTS; PR00658; CD44.
 DR Pfam; PD000918; Link; 1.
 DR SMART; SM00445; Link; 1.
 DR PROSITE; PS01241; Link; 1.
 KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
 KW Proteoglycan; Signal; Alternative splicing;
 KW Pyroglutamate; Pyroglutamate; Pyroglutamate;
 FT SIGNAL 1 21
 FT CHAIN 22 503 CD44 ANTIGEN.
 FT DOMAIN 22 410 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 411 431 POTENTIAL.
 FT DOMAIN 432 503 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 51 123 LINK.
 FT DOMAIN 154 162 ARG/LYS-RICH (BASIC).
 FT DOMAIN 228 410 STEM.
 FT MOD_RES 22 22 PYROGLUTAMATE CARBOXYLIC ACID (PROBABLE).
 FT DISUFID 56 122 BY SIMILARITY.
 FT DISUFID 80 100 BY SIMILARITY.
 FT MOD_RES 433 433 PHOSPHORYLATION (BY PKC) (PARTIAL) (BY
 FT MOD_RES 467 467 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 467 467 PHOSPHORYLATION (PARTIAL) (BY
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPIC 224 385 LATPWVSAHTKQKQRTQWPHNSPEVLLQTTTMTDID
 RNSTSAHGNWNTQEPQPPFNHBYQDBEETPHATSTTWD
 NSTPRAATQKFWENWQGNKPTPSBDSHVTEGTASA
 HNNHPQRTVTSQEDVSWTDFDPFISHPMQGHQTESK
 -> SDGSSMDPRGFDVTHTGSELA (in isoform
 1)).
 FT ID=VSP_005330.
 FT R -> S (IN REF. 2).
 FT CONFLICT 74 74
 FT SEQUENCE 503 AA; 55945 MW; FB489D009B4E22 CRC64;

Query Match 7.8%; Score 86; DB 1; Length 503;
 Best Local Similarity 20.7%; Pred. No. 2.5;
 Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPTSLAPPMDPSPIWIIIGVIFCIIVAILLSIGWQRR-----171
 DB 396 VITTSPPARRPQIPEWLLI---LASLALAIIVACIANSRRRCKQKLVNSGNGTV 452
 QY 172 KNEKPEVDVDAEKCENMTIENGIPSD-----PLDMKGGI 207
 DB 453 EDRKPSLNGEASKSQEWHVANKETETPDQFWTADETNLSQVDMKIGV 503

RESULT 11
 FLIP_BACSU

ID AC P23447;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DR Flagellar M-ring protein.
 GN FLIP OR BSU16210.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91285431; PubMed=1905667;
 RA Zuberi A.R., Ying C., Bischoff D.S., Ordal G.W.;
 RT "Gene-protein relationships in the flagellar hook-basal body complex
 of Bacillus subtilis: sequences of the flgB, flgC, flgE and
 flgF genes.";
 RL Gene 101:23-31 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=9804033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari B., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Goleightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lepidine A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche S., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256 (1997).
 RN [3]
 RP SEQUENCE OF 355-536 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=91258343; PubMed=1828465;
 RA Albertini A.M., Caramori T., Crabb W.D., Scoffone F., Galizzi A.;
 RT "The flaa locus of Bacillus subtilis is part of a large operon coding
 for flagellar structures, motility functions, and an ATPase-like
 polypeptide.";
 RL J. Bacteriol. 173:3573-3579 (1991).
 CC -!- FUNCTION: The M ring may be actively involved in energy
 transduction.
 CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
 FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
 MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER
 MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD
 VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO
 THE M RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE
 PERIPLASMIC SPACE, RESPECTIVELY.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated.
 CC -!- SIMILARITY: Belongs to the flgF family.

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EMBL; M54965; -; NOT ANNOTATED_CDS.
EXBL; Z99112; CAB13494.1; -;
EXBL; X56049; CAA339520.1; -;
DR PIR; JG0022; JG0022; flif.
DR Subtilisin; BG10240; flif.
DR InterPro; IPR000067; FlgMing FLIF.
DR InterPro; IPR006182; YscJ FLIF.
DR Pfam; PF01514; YscJ FLIF; 1.
DR PRINTS; PR01009; FLGMRINGFLIF.
DR TIGRFAMs; TIGR00206; flif; 1.
KW Flagellum; Membrane; Complete proteome.
SQ SEQUENCE 536 AA; 5930 MW; 21110D4C7CF1927A CRC64;

Query Match 7.7%; Score 84.5; DB 1; Length 536;
Best Local Similarity 19.9%; Pred. No. 3.7;
Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;

Qy 9 VTAHAEICQGAENAFKRLSIRLTALGDKAYADTHEEVLFKAWAFSMRKVPNREATE 68
D5 352 VNRHKET-----AESPKVR-----DLGIQNVVEPPDAKNTASLTERQDD 393
Qy 69 ISHVLNCNVTORGVFWFVTPDSKNHTLEAVEVOSAIRMNKNRINNAFFLNDQTLFLKI 128
D5 394 IQKIL--STVVRTS---LDKDTQNQLSDADINNKLVSVQPFQGVNLDNTEER--- 444
Qy 129 PSTLAPPMDPSVPIW-IIIFGVICIIIVAIILGILGWORRRNKEPSVDDAEKCE 187
D5 445 -----SSGIPLWAYVGGVLAATVLIIMLI-----RKRAQEDFEFEYEYE-- 487
Qy 188 NWITIENGIPSPDLDLM 203
D5 488 -----VPOEPINL 495

RESULT 12
ID_PTPRJ HUMAN STANDARD; PRT; 1337 AA.
AC Q12913; Q15255; Q8NEM2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTp eta) (Protein-tyrosine phosphatase receptor type J) (Density
DE enhanced phosphatase-1) (DEP-1) (CD148 antigen).
GN PTPRJ OR DEPI
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1] _SEQUENCE FROM N.A.
RX MEDLINE=95024024; PubMed=7937872;
RA Oestman A., Yang Q., Tonks N.K.;
RT Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
RT is enhanced with increasing cell density.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
[2]
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
RT Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, HPTp eta.;
RL Blood 84:4186-4194(1994).
[3]

RP TISSUE=Colon;
RX MEDLINE=22084388; PubMed=12089527;
RA Ruitenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vicek C.,
RA Cuiwen T., Klous A.M., Tripodis N., Perrakis A., Boerrigter L.,
RA Groot P.C., Lindeman J., Mooi W.J., Meijer G.A., Scholten G.,
RA Dauwerse H., Faces V., van Zandwijk N., van Ommen G.J.B., Demant P.;
RT Ptpj is a candidate for the mouse colon-cancer susceptibility locus
RT Sccl and is frequently deleted in human cancers.;
RL Nat. Genet. 31:295-300(2002).
CC -!- FUNCTION: May contribute to the mechanism of contact inhibition of
CC cell growth.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate. Type I membrane protein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: N- and O-glycosylated.
CC -!- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and
CC breast.
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd148.htm".

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EMBL; U10886; AAB36687.1; -;
EMBL; D37781; BAA07035.1; -;
EMBL; AF387844; AAM69432.1; JOINED.
EMBL; AF387823; AAM69432.1; JOINED.
EMBL; AF387824; AAM69432.1; JOINED.
EMBL; AF387825; AAM69432.1; JOINED.
EMBL; AF387826; AAM69432.1; JOINED.
EMBL; AF387827; AAM69432.1; JOINED.
EMBL; AF387828; AAM69432.1; JOINED.
EMBL; AF387829; AAM69432.1; JOINED.
EMBL; AF387830; AAM69432.1; JOINED.
EMBL; AF387831; AAM69432.1; JOINED.
EMBL; AF387832; AAM69432.1; JOINED.
EMBL; AF387833; AAM69432.1; JOINED.
EMBL; AF387834; AAM69432.1; JOINED.
EMBL; AF387835; AAM69432.1; JOINED.
EMBL; AF387836; AAM69432.1; JOINED.
EMBL; AF387837; AAM69432.1; JOINED.
EMBL; AF387838; AAM69432.1; JOINED.
EMBL; AF387839; AAM69432.1; JOINED.
EMBL; AF387840; AAM69432.1; JOINED.
EMBL; AF387841; AAM69432.1; JOINED.
EMBL; AF387842; AAM69432.1; JOINED.
EMBL; AF387843; AAM69432.1; JOINED.
PIR; I38670; I38670.
HSPF; P18052; I1FPO.
DR GENE; HGNC:9673; PTPRJ.
DR MIN; 600925; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho...; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin...; TAS.
DR InterPro; IPR008957; FN iii-like.
DR InterPro; IPR003961; FN iii.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00041; fn3_6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPRJPHPTASE.
DR SMART; SM00060; FN3; 8.


```

FT CA_BIND 377 385 POTENTIAL.
FT CA_BIND 441 449 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 437 439 BY SIMILARITY.
FT DISULFID 81 88 BY SIMILARITY.
FT DISULFID 132 153 BY SIMILARITY.
FT DISULFID 169 182 BY SIMILARITY.
FT DISULFID 489 500 BY SIMILARITY.
FT DISULFID 506 562 BY SIMILARITY.
FT DISULFID 623 629 BY SIMILARITY.
FT DISULFID 695 708 BY SIMILARITY.
FT DISULFID 849 905 INTERCHAIN (BY SIMILARITY).
FT DISULFID 910 915 BY SIMILARITY.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 587 587 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 701 701 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 719 719 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 751 751 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 762 762 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 818 818 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 877 877 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 904 904 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 952 952 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1044 AA; 116141 MW; 3D59A318B51320CE CRC64;

Query Match 7.5%; Score 82.5; DB 1; Length 1044;
Best Local Similarity 21.3%; Pred. No. 12;
Matches 38; Conservative 28; Mismatches 59; Indels 53; Gaps 8;

Qy 17 COPG-AENAFKRLSIRLALGDKAYAMDTHREYLFKAMVAFPMKVPNREATEISHVLLC 75
Dz 915 CNVGQLRGKSAALKIRSLRAETLAEFLQKNDPPTLSSNVSPKVKMPK----- 963
Qy 76 NVTQVSEFWVVTDPSPKQHTLPALVEVQSAIPMKNRINNAPFENDQTLFLKIPSTLAPP 135
Db 964 -----VQPAK---LP--EGSTAIRTS-----VINST--PN 986

Qy 136 MDPSPVPIIIFGFCIIIVAILLIU--SGIWRKRKNKEPSEVDDAEDKCNEMIT 191
Dz 987 VSFVIPLWIIILAIMLGLLVLAVLTALWKCGFFDRAPPDQ--DMADREQLTNNKTT 1042

RESULT 14
ITAH HUMAN STANDARD; PRT; 1189 AA.
AC Q9UKX5; Q9UKQ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin alpha-11 precursor.
GN ITGA11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart, and Osteoblasts;
RX MEDLINE=99417678; PubMed=10486209;
RA Lehnert K., Ni J., Leung E., Gough S.M., Weaver A., Yao W.P., Liu D.,
RA Wang S.-X., Morris C.M., Krissansen G.W.;
RT "Cloning, sequence analysis, and chromosomal localization of the novel
RL human integrin alpha11 subunit (ITGA11).";
RN Genomics 60:179-187(1999).
RP [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Fetal muscle, and Uterus;

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RX MEDLINE=99395147; PubMed=10464311;
RA Velling T., Kusche-Gullberg M., Seijersen T., Gullberg D.;
RT "cDNA Cloning and Chromosomal Localization of Human alpha(11)
RT Integrin. A collagen-binding, i domain-containing, beta(1)-associated
RL integrin alpha-chain present in muscle tissues.";
RN J. Biol. Chem. 274:25735-25742(1999).
[3]
RC SEQUENCE OF 954-1188 FROM N.A.
RC TISSUE=Fibroblast;
RA Andreu N., Estivill X., Escarceller M., Sumoy L.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: INTEGRIN ALPHA-11/BETA-1 IS A RECEPTOR FOR COLLAGEN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-11
CC ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: ACCORDING REF.2 HIGHEST LEVELS IN UTERUS AND
CC HEART. INTERMEDIATE LEVELS IN SKELETAL MUSCLE AND INTERMEDIATE TO
CC LOW LEVELS IN PANCREAS, KIDNEY AND PLACENTA. ACCORDING REF.1 ALSO
CC FOUND IN BRAIN, COLON, LUNG, SMALL INTESTINE, STOMACH, TESTIS,
CC SALIVARY GLANDS, THYROID GLANDS AND PROSTATE. VERY LOW LEVELS IN
CC PERIPHERAL BLOOD LYMPHOCYTES, FETAL BRAIN AND FETAL LIVER.
CC -!- DEVELOPMENTAL STAGE: STRONGLY UP-REGULATED IN DIFFERENTIATING
CC FETAL MUSCLE CELLS (IN VITRO).
CC -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
EMBL; AF109681; AA01258.1; .
EMBL; AF131378; AD051919.2; .
EMBL; AL359064; CAB94392.1; .
HSSP; P17301; IAOX.
DR Genew; HGNC:6136; ITGA11.
DR MIM; 604789; .
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0007517; P:muscle development; TAS.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00032; vwa; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; FALSE_NEG.
DR PROSITE; PS0234; VWFA; 1.
KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Signal; Repeat; Calcium; Magnesium; Polymorphism.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1189 INTEGRIN ALPHA-11.
FT DOMAIN 23 1142 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1143 1165 POTENTIAL.
FT DOMAIN 1166 1189 CYTOPLASMIC (POTENTIAL).
FT REPEAT 38 94 FG-GAP 1.
FT REPEAT 102 163 FG-GAP 2.
FT DOMAIN 167 345 VWFA.
FT REPEAT 359 420 FG-GAP 3.
FT REPEAT 422 475 FG-GAP 4.
FT REPEAT 477 537 FG-GAP 5.
FT REPEAT 539 598 FG-GAP 6.
FT REPEAT 601 653 FG-GAP 7.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:23:49 ; Search time 45 Seconds
(without alignments)
1486.441 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102

Sequence: 1 MLWLLFFLVTAHAEICQPG.....ENGIPSDPLMKGGILWMP8 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying Chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_protein:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	97.4	222	4 Q9HBJ8	Q9HBJ8 homo sapien
2	928	84.2	222	11 Q9ESG4	Q9ESG4 mus musculus
3	921	83.6	222	11 Q9ESG3	Q9ESG3 rattus norv
4	376	34.1	804	4 Q9UF26	Q9UF26 homo sapien
5	376	34.1	805	4 Q9NR77	Q9NR77 homo sapien
6	376	34.1	816	4 Q9WTO0	Q9WTO0 homo sapien
7	373	33.8	805	4 Q9SYF1	Q9SYF1 homo sapien
8	361	32.8	805	11 Q9R010	Q9R010 mus musculus
9	357	32.4	265	11 Q9D836	Q9D836 mus musculus
10	357	32.4	798	11 Q99N71	Q99N71 mus musculus
11	100	9.1	1053	5 Q8TAQ8	Q8TAQ8 plasmodium
12	97.5	8.8	1086	5 Q18428	Q18428 geodia cydo
13	96.5	8.8	543	11 Q8C0H7	Q8C0H7 mus musculus
14	96.5	8.8	1012	11 Q70304	Q70304 mus musculus
15	95.5	8.7	1406	13 Q9W6V5	Q9W6V5 gallus gall
16	93.5	8.5	929	5 Q9VR32	Q9VR32 drosophila

RESULT 1

Q9HBJ8 PRELIMINARY, PRT; 222 AA.

ALIGNMENTS

17	91.5	8.3	823	11	Q8CE84	Q8CE84 mus musculus
18	91.5	8.3	1188	11	Q7TQC3	Q7TQC3 mus musculus
19	90	8.2	716	11	Q8C449	Q8C449 mus musculus
20	90	8.2	754	11	Q9BRK4	Q9BRK4 mus musculus
21	89.5	8.1	161	11	Q9WUP8	Q9WUP8 rattus norv
22	89.5	8.1	244	10	Q9C6E1	Q9C6E1 arabidopsis
23	89.5	8.1	1188	5	Q76326	Q76326 drosophila
24	89	8.1	1054	5	Q9U6S1	Q9U6S1 strongyloce
25	88.5	8.0	656	12	Q9QU36	Q9QU36 tiv-like mi
26	88	8.0	580	11	Q80X37	Q80X37 mus musculus
27	87	7.9	498	11	Q9D001	Q9D001 mus musculus
28	87	7.9	716	11	Q8C375	Q8C375 mus musculus
29	87	7.9	1326	2	Q9GHJ4	Q9GHJ4 aeromonas p
30	86.5	7.8	252	10	Q9FX00	Q9FX00 arabidopsis
31	86.5	7.8	956	5	Q9W4T9	Q9W4T9 drosophila
32	86.5	7.8	1063	16	Q8KXCX	Q8KXCX chlorobium
33	86	7.8	364	11	Q70509	Q70509 rattus norv
34	86	7.8	780	11	Q08779	Q08779 rattus norv
35	85.5	7.8	667	10	Q9M3D7	Q9M3D7 arabidopsis
36	85.5	7.8	826	4	Q8IY15	Q8IY15 homo sapien
37	85.5	7.8	959	5	Q9N9Y9	Q9N9Y9 drosophila
38	85.5	7.8	975	5	Q97174	Q97174 drosophila
39	85.5	7.8	1148	4	Q9H7S7	Q9H7S7 homo sapien
40	85.5	7.8	1488	4	Q9HQM3	Q9HQM3 homo sapien
41	84.5	7.7	252	10	Q9FGB3	Q9FGB3 arabidopsis
42	84.5	7.7	468	16	Q9JVK7	Q9JVK7 neisseria m
43	84.5	7.7	823	4	Q8WYI8	Q8WYI8 homo sapien
44	84.5	7.7	1033	13	Q42598	Q42598 xenopus lae
45	84.5	7.7	1112	5	Q02344	Q02344 caenorhabdi

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RA [3]
RA SEQUENCE FROM N.A.
RA TISSUE=Bone marrow, Colon, and Kidney;
RA Strausberg R.;
RA Submitted (AFR-2003) to the EMBL/GenBank/DBJ databases.
RA EMBL; AF229179; AAG09466.1; -
RA EMBL; BC015099; AAH15099.1; -
RA EMBL; BC014317; AAH14317.1; -
RA EMBL; BC056606; AAH50606.1; -
RA Hypothetical protein.
RA SEQUENCE 222 AA; 25335 MW; 52C0ED522134ED05 CRC64;
RA
RA Query Match 97.4%; Score 1073; DB 4; Length 222;
RA Best Local Similarity 100.0%; Pred. No. 2.7e-105;
RA Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLLWFLFLVTAIHAEELCPGAEAFKVRISIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60
DB 1 MLLWFLFLVTAIHAEELCPGAEAFKVRISIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60
QY 61 VPNEATEISHVLLCNVTQRFVFWVVDPSKNHTLPAVEQSAIRNKNRINNAFFLND 120
DB 61 VPNEATEISHVLLCNVTQRFVFWVVDPSKNHTLPAVEQSAIRNKNRINNAFFLND 120
QY 121 QTLFELKIPSTLAPPMDPSVPIIIFGVIFCIITVAIALILSGIWRORRKNKEPSEVD 180
DB 121 QTLFELKIPSTLAPPMDPSVPIIIFGVIFCIITVAIALILSGIWRORRKNKEPSEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGG 206
DB 181 DAEDKCNMTIENGIPSDPLDMKGG 206
RA
RA RESULT 2
RA Q9ESG4
RA ID Q9ESG4 PRELIMINARY; PRT; 222 AA.
RA
RA AC Q9ESG4
RA DT 01-MAR-2001 (TrEMBLrel. 16, Created)
RA DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
RA DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
RA DE Kidney-specific membrane protein NK-17 (0610008J07Rik protein).
RA GN NK17 OR 0610008J07R1K.
RA OS Mus musculus (Mouse).
RA OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RA OX NCBI_TaxID=10090;
RA RN [1]
RA RP SEQUENCE FROM N.A.
RA RC STRAIN=ICR;
RA RX MEDLINE=99362608; PubMed=10432394;
RA RA Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
RA Shikata K., Makino H.;
RA RT "Screening for genes up-regulated in 5/6 nephrectomized mouse
RA kidney.";
RA RL Kidney Int. 56:549-558(1999).
RA RN [2]
RA RP SEQUENCE FROM N.A.
RA RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA RX MEDLINE=21085660; PubMed=11217851;
RA RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gajobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

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RA Sakai L.M., Tomita R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Sait C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RA [3]
RA SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Kidney;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Li X., Gibbs R.A.,
RA Whiting M., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RA [4]
RA SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RA EMBL; AF178085; AAG09306.1; -
RA EMBL; AK002337; BAB22022.1; -
RA EMBL; BC049912; AAH49912.1; -
RA MGI:1926234; NXL17.
RA SQ SEQUENCE 222 AA; 25070 MW; C07E732CE92935A9 CRC64;
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RA Query Match 84.2%; Score 928; DB 11; Length 222;
RA Best Local Similarity 84.5%; Pred. No. 6e-90;
RA Matches 174; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
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QY 1 MLLWFLFLVTAIHAEELCPGAEAFKVRISIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60
DB 1 MLLWFLFLVTAIHAEELCPGAEAFKVRISIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60
QY 61 VPNEATEISHVLLCNVTQRFVFWVVDPSKNHTLPAVEQSAIRNKNRINNAFFLND 120
DB 61 VPNEATEISHVLLCNVTQRFVFWVVDPSKNHTLPAVEQSAIRNKNRINNAFFLND 120
QY 121 QTLFELKIPSTLAPPMDPSVPIIIFGVIFCIITVAIALILSGIWRORRKNKEPSEVD 180
DB 121 HTLEFLKIPSTLAPPMDPSVPIIIFGVIFCIITVAIALILSGIWRORRKNKEPSEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGG 206
DB 181 DAEDKCNMTIENGIPSDPLDMKGG 206
RA
RA RESULT 3
RA Q9ESG3 PRELIMINARY; PRT; 222 AA.
RA AC Q9ESG3;

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DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE Kidney-specific membrane protein NK-17.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99362608; PubMed=10432394;
 RA Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
 RA Shikata K., Makino H.;
 RT "Screening for genes up-regulated in 5/6 nephrectomized mouse
 RT kidney";
 RL Kidney Int. 56:549-558(1999).
 DR EMBL: AF178086; AAGO9307.1; -.
 DR EMBL: AF178086; AAGO9307.1; -.
 SQ SEQUENCE 222 AA; 25226 MW; 7P4E166AE344F855 CRC64;

 Query Match 83.6%; Score 921; DB 11; Length 222;
 Best Local Similarity 84.5%; Pred. No. 3.3e-89;
 Matches 174; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

 QY 1 MLWLFFLVTAHAEICQGAENAFKVRISITLALGDKAYAWDTNVEYLFAKAWAFSMRK 60
 DQ 1 MLWLFFLVTAHAEICQGAENAFKVRISITLALGDKAYAWDTNVEYLFAKAWAFSMRK 60
 QY 61 VNRREATEISHVLLCNVTVQSFVFWVVDPSKNHTLPVEVQSAIRMNKRINNAFFLND 120
 DQ 61 VNRREATEISHVLLCNVTVQSFVFWVVDPSKNHTLPVEVQSAIRMNKRINNAFFLND 120
 QY 121 QTLFLFKIPSTLAPPDPSVPIWIIIFGVICIIIVAIALLILSGIWRQRNKEPSEVD 180
 DQ 121 HTLEPLFKIPSTLAPPDPSVPIWIIIFGVICIIIVAIALLILSGIWRQRNKEPSEVD 180
 QY 181 DAEDKCNITTIENGIPSPDLNKGK 206
 DQ 181 DAEDKCNITTIENGIPSPDLNKGK 206

 RESULT 4
 Q9UFZ6 PRELIMINARY; PRT; 804 AA.
 AC Q9UFZ6;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKF2P34A014.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Wambout K., Reubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL110224; CAB53682.1; -.
 DR PIR: T14762; T14762.
 DR MEROPS: M02.006; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004246; F:peptidyl-diesterase A activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR InterPro: IPR006025; Pept M Zn BS.
 DR Pfam: PF01401; Peptidase M2; 1.
 DR PRINTS: PR00791; PEPDPTASEA.
 DR PRODOM: PD004184; Peptidase M2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Hypothetical protein.

FT NON TER 1
 SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

 Query Match 34.1%; Score 376; DB 4; Length 804;
 Best Local Similarity 47.9%; Pred. No. 8.2e-31;
 Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

 QY 19 PGAENAFKVRISITLALGDKAYAWDTNVEYLFAKAWAFSMR---KVENREAT-EISHVL 73
 DQ 19 PGAENAFKVRISITLALGDKAYAWDTNVEYLFAKAWAFSMR---KVENREAT-EISHVL 73
 DQ 611 PYAQSIKVRISITLALGDKAYAWDTNVEYLFAKAWAFSMR---KVENREAT-EISHVL 670
 QY 74 LCNVTVQSFVFWVVDPSKNHTLPVEVQSAIRMNKRINNAFFLNDOTLEFLKIPSTL 132
 DQ 74 LCNVTVQSFVFWVVDPSKNHTLPVEVQSAIRMNKRINNAFFLNDOTLEFLKIPSTL 132
 DQ 671 VANLKPRISFNFVTAPEQVSDIIPRTEVEKAIARMSRINDAFRLNDSLEFLGIQPTL 730
 QY 133 APPMDPSVPIWIIIFGVICIIIVAIALLILSGIWRQRNKEPS 177
 DQ 133 APPMDPSVPIWIIIFGVICIIIVAIALLILSGIWRQRNKEPS 177
 DQ 731 GFPNQPPVSIWIIIFGVVGVVGVIVILFTGIEDRKKKARS 775

 RESULT 5
 Q9NRA7 PRELIMINARY; PRT; 805 AA.
 AC Q9NRA7;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Angiotensin converting enzyme-like protein (ACE-related
 DE carboxypeptidase ACE2) (Angiotensin I converting enzyme
 DE (Peptidyl-diesterase A) 2).
 GN HOMO
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Lymphoma;
 RA Tipnis S.R., Hooper N.M., Hyde R.J., Christie G., Karran E.,
 RA Turner A.J.;
 RT "A Human Homolog of Angiotensin Converting Enzyme - Cloning and
 RT Functional Expression As A Captopril-Inensitive Carboxypeptidase";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
 RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
 RA Breitbart R.E., Acton S.;
 RT "A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to
 RT angiotensin-1-9";
 RL Circ. Res. 0:0-0(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF241254; AAF78220.1; -.
 DR EMBL: AF241254; AAF78220.1; -.
 DR EMBL: AY217547; AA025651.1; -.
 DR MEROPS: M02.006; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO: GO:0004246; F:peptidyl-diesterase A activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR InterPro: IPR006025; Pept M Zn BS.
 DR Pfam: PF01401; Peptidase M2; 1.
 DR PRINTS: PR00791; PEPDPTASEA.
 DR PRODOM: PD004184; Peptidase M2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Carboxypeptidase.


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SQ SEQUENCE 805 AA; 92462 MW; 3EE6BE0A931550B8 CRC64;
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 8.2e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRIITALGDKAYADTNEEYLFKAMVAFSMR-----KVPNREAT-EISHVL 73
DQ 612 PYAQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEEDVR 671
QY 74 LCNVTQVSVFVVTDPK-NHTLPAVEVQSARIMKNRINNAFFINDQTLFELKIPSTL 132
DQ 672 VANLKPRISENFVVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731

QY 133 APPMDPSVPIWIIIFGVFCIIIVAILLISGIWQRRKKNKPS 177
DQ 732 GPPNPQPPSVIWLIVFGVGMGVIVGVILIFTGIRDRKKKNKARS 776

RESULT 6
Q86WT0 PRELIMINARY; PRT; 816 AA.
AC Q86WT0
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to angiotensin I converting enzyme (Peptidyl-dipeptidase A) 2
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC048094; AAH48094.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDASEA.
DR PRODOM; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
FT NON_TER
SQ SEQUENCE 816 AA; 93516 MW; EFBD58B3DA2EDF3 CRC64;
Query Match 34.1%; Score 376; DB 4; Length 816;
Best Local Similarity 47.9%; Pred. No. 8.3e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRIITALGDKAYADTNEEYLFKAMVAFSMR-----KVPNREAT-EISHVL 73
DQ 623 PYAQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEEDVR 682
QY 74 LCNVTQVSVFVVTDPK-NHTLPAVEVQSARIMKNRINNAFFINDQTLFELKIPSTL 132
DQ 683 VANLKPRISENFVVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 742

QY 133 APPMDPSVPIWIIIFGVFCIIIVAILLISGIWQRRKKNKPS 177
DQ 743 GPPNPQPPSVIWLIVFGVGMGVIVGVILIFTGIRDRKKKNKARS 787

RESULT 7
Q8BYF1 PRELIMINARY; PRT; 805 AA.
ID Q8BYF1
AC Q8BYF1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ACE2.
GN ACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Komatsu T.; Suzuki Y.; Sugano S.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC Suzuki Y.; Watanabe M.; Sugano S.;
RA *cloning, expression analysis and chromosomal localization of a novel
RT ACE like enzyme.
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046569; BAB40370.1; -.
DR MEROPS; M02.006; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept_M2n_BS.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDASEA.
DR PRODOM; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72 CRC64;
Query Match 33.8%; Score 373; DB 4; Length 805;
Best Local Similarity 47.3%; Pred. No. 1.7e-30;
Matches 78; Conservative 33; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRIITALGDKAYADTNEEYLFKAMVAFSMR-----KVPNREAT-EISHVL 73
DQ 612 PYAQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEEDVR 671
QY 74 LCNVTQVSVFVVTDPK-NHTLPAVEVQSARIMKNRINNAFFINDQTLFELKIPSTL 132
DQ 672 VANLKPRISENFVVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731

QY 133 APPMDPSVPIWIIIFGVFCIIIVAILLISGIWQRRKKNKPS 177
DQ 732 GPPNPQPPSVIWLIVFGVGMGVIVGVILIFTGIRDRKKKNKARS 776

RESULT 8
Q8RO10 PRELIMINARY; PRT; 805 AA.
ID Q8RO10
AC Q8RO10
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 2010305L05 gene.
GN ACE2 OR 2010305L05R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC026801; AAH26801.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
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DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001548; Peptidase_M2.
DR InterPro: IPR006025; Pept_M2n_RS.
DR InterPro: IPR001580; WD40.
DR Pfam: PF01401; Peptidase_M2; 1.
DR PRINTS: PR00791; PEPDIP7AEEA.
DR ProDom: PD004184; Peptidase_M2; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
Query Match 32.8%; Score 361; DB 11; Length 805;
Best local Similarity 40.9%; Pred. No. 3.2e-25;
Matches 81; Conservative 35; Mismatches 52; Indels 30; Gaps 5;
QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNBEYLFKAMVAFSMRK-----VFNREATEI 69
Db 612 PYADQSIKVRISLKSALGANAYEWNTNEMFLFRSSVAYAMRYKVFSTIKNTVPFLE---- 667
QY 70 SHVLNCNTQVRSFVFWVVDPSK-NHTLPAVEQSAIRMKNNRINNAPFLNDOTLEFLKI 128
Db 568 EDVRVSDLKRVSYFFVFTSPQNSVDVPRSEVEDAIRMSGRINDVFGDMSLEFLGI 727
QY 129 PSTLAPPMDPSVPIIIFGVFCIIIVAILLISGIMQRRRNKPESEVDDAEKCN 188
Db 728 HPTLEPPYQPPVTIWLIFGVWALVVVGIIILVTGKGRKKNETKRE----- 777
QY 189 MITEENGIPSDPLDKCG 206
Db 778 ----EN--PYDSMDIGK 789
RESULT 9
Q9D836 PRELIMINARY; PRT; 265 AA.
AC Q9D836;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Adult male small intestine cDNA, RIKEN full-length enriched library,
DE clone:2010305L05 product:ANIGOTENSIN-converting enzyme-related
DE carboxypeptidase, full insert sequence (fragment).
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=22354583; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[4]
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[5]
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[6]
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Tamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK008530; BAB25723.2; -.
DR MGD; MGI:1917258; Ace2.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001548; Peptidase_M2.
DR Pfam: PF01401; Peptidase_M2; 1.
FT NON_TER
SQ SEQUENCE 265 AA; 30078 MW; 2A02B2CE3817C76C CRC64;
Query Match 32.4%; Score 357; DB 11; Length 265;
Best local Similarity 44.1%; Pred. No. 2.2e-29;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;
QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNBEYLFKAMVAFSMRK-----VFNREATEI 69
Db 72 PYADQSIKVRISLKSALGANAYEWNTNEMFLFRSSVAYAMRYKVFSTIKNTVPFLE---- 127
QY 70 SHVLNCNTQVRSFVFWVVDPSK-NHTLPAVEQSAIRMKNNRINNAPFLNDOTLEFLKI 128
Db 128 EDVRVSDLKRVSYFFVFTSPQNSVDVPRSEVEDAIRMSGRINDVFGDMSLEFLGI 187
QY 129 PSTLAPPMDPSVPIIIFGVFCIIIVAILLISGIMQRRRNKPESE 178
Db 188 HPTLEPPYQPPVTIWLIFGVWALVVVGIIILVTGKGRKKNETKRE 237
RESULT 10
Q99N71 PRELIMINARY; PRT; 798 AA.
ID Q99N71
AC Q99N71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anigotensin-converting enzyme-related carboxypeptidase.
GN 2010305L05RIK OR ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RA Kometani T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y.,
RP SEQUENCE FROM N.A.
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB053181; BAB40431.1; -.
DR MEROPS; M02.006; -.
DR MGD; MGI:1917258; Ace2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004180; P:carboxypeptidase activity; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Carboxypeptidase.
SQ SEQUENCE 798 AA; 91943 MW; 403A8A29D55725A4 CRC64;

Query Match 32.4%; Score 357; DB 11; Length 798;
Best Local Similarity 44.1%; Pred. No. 8.3e-29;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;

QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNEEYLKAWAFVSRK-----VNPKEATEI 69
Db 612 PYAQSIKVRISLKALCANAYTNNEMFLRSVAYAKYPSIIKQTVPPLE---- 667
QY 70 SHVLLCNVTQVSWFWVTDSK-NHTLPVAVQSAIRMNKRNNAFFNDQTLLEFKI 128
Db 668 EDVRSVLKPRVSYFFFTSPQNSVDVIPRSEVDAIRMSGRINDVFGNDNSLEFLGI 727
QY 129 PSTLAPMDPSVPTWIIIFGIFCIIIVAIALLILSGIWRRRNKPESE 178
Db 728 HPTLEPPYQPPVTWIIIFGVVMAVVGVIIIVTGTGKGRKKNETKRE 777

RESULT 11
Q81AQ8 PRELIMINARY; PRT; 1053 AA.
ID AC Q81AQ8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vacuolar proton-translocating ATPase subunit A, putative.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51303.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase subunit 1.
DR Pfam; PF01496; V_ATPase_sub_a; 1.
SQ SEQUENCE 1053 AA; 152998 MW; 8B9F2559D3FC3F08 CRC64;

Query Match 9.1%; Score 100; DB 5; Length 1053;
Best Local Similarity 21.3%; Pred. No. 0.19;
Matches 43; Conservative 31; Mismatches 72; Indels 56; Gaps 8;

QY 22 ENAFKVLRSIRLTALGDKAYAWDTNEEYLKAWAFVSRKVPNREATEISHVLLC----- 75

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Db 330 EHAQGLKELRIINDKEXALYAEYFNEIFVLINVVPEKNSLIEEWKLFCKKERHI 1389
QY 76 -----NVTQVSWFWVTDSK-NHTLPVAVQSAIRMNKRNNAFFNDQTL- 123
Db 390 YANLNYFEQSDITLRCWYSANDEKIRHIL-----INKSSNDLVALLSKILR 441
QY 124 -----EFLK-----IPSTLAPP-----MDPSVPTWIIIFGVIF- 153
Db 442 FNVSPPTVYKTNEFTKSYQSMVDTYGVPRYGEINPAISTIIIFPFLFGIMYGVGHGLCI 501
QY 154 IIVAIALLILSGIWRRRNKKE 175
Db 502 FLFALFLIIMNKNVKNKNNE 523

RESULT 12
O18428 PRELIMINARY; PRT; 1086 AA.
ID AC O18428
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Integrin.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demosporangia; Tetractinomorpha;
OC Astrophorida; Geodidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97254987; PubMed=9100369;
RA Pancer Z., Kruse M., Mueller I., Mueller W.B.G.;
RT "On the origin of adhesion receptors of metazoa: Cloning of the
RT integrin alpha subunit cDNA from the sponge Geodia cydonium.";
RL Mol. Biol. Evol. 14:391-398 (1997).
DR EMBL; X97283; CAA65943.1; -.
DR PIR; T18523; T18523.
DR GO; GO:000305; C:integrin complex; IEA.
DR GO; GO:0004895; P:cell adhesion receptor activity; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Int_alpha; 4.
SQ SEQUENCE 1086 AA; 118628 MW; 269189D0364DBFA5 CRC64;

Query Match 8.8%; Score 97.5; DB 5; Length 1086;
Best Local Similarity 25.5%; Pred. No. 0.37;
Matches 36; Conservative 24; Mismatches 52; Indels 29; Gaps 6;

QY 63 NREATEISHVL---LCNVTQVSWFWVTDSKHTLPVAVQSAIRMNKRNNAFFL 118
Db 963 NRQVQVISAVIDERHAGIDSYTF-----PSAQ-----VEMVGSDHINESYTKD 1007
QY 119 NDQTLLEFLKIPSTLAPP-----DPSVPTWIIIFGIFCIIIVAIALLILSGIWRRRNK 173
Db 1008 NNASAEFRSIPGLVVPVSGSGDSEVPVVIAPVIAAVIIVVAVVLYFCGFRKKN 1067
QY 174 KEPSVDDAEDKCNMTIEN 194
Db 1068 KQ-----SIEDQARENLABEN 1083

RESULT 13
Q8COH7 PRELIMINARY; PRT; 543 AA.
ID AC Q8COH7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha 8 integrin (Fragment).
GN A1447669
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK031326; BAC27348.1; -
 DR MGI; MGI:2138946; AI447669.
 DR GO; GO:0008305; C:integrin complex; IEA.
 DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
 DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF00357; Integrin_A; 1.
 DR PRINTS; PR01185; INTEGRIN_A.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 FT NON_TER 1
 SQ SEQUENCE 543 AA; 61249 MW; 430DCB3279A8FD4 CRC64;
 Query Match 8.8%; Score 96.5; DB 11; Length 543;
 Best Local Similarity 22.0%; Pred. No. 0.2;
 Matches 37; Conservative 32; Mismatches 40; Indels 59; Gaps 8;
 QY 20 GAENAFKVLRSIRLTALGDKAYADMTNEEYLFKAMVAFSMKVPNREATEISHVLLCNVTQ 79
 DB 421 GGSAY--LKVRSRLWAHTFLKRNNDHYALASLVSEVKMPYKE----- 463
 QY 80 RVSEFWVTDPSPKNTLPA--VEVQSAIRMNKNRINNNAFFLNDQTLFLKIPSTLAPPMD 137
 DB 464 -----QPAK--LPAGSTAVKTSV-----IWAT--PNVS 487
 QY 138 PSVFIMIIIFGVIFCIIIVAILLIL--SGIWORRRKNKEPSEVDDAE 183
 DB 488 PSIFLWVILAILLGLLVAILTLALWKCGFFDRARPPQD--EMTDRE 533
 RESULT 14
 O70304
 ID O70304 PRELIMINARY; PRT; 1012 AA.
 AC O70304;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 D3 Integrin alpha8 (Fragment).
 GN ITGA8.
 OS Mus musculus (Mouse).
 OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97207007; PubMed=9054500;
 RA Muller U., Wang D., Denda S., Meneses J.J., Pedersen R.A.,
 RA Reichardt L.F.;
 RT "Integrin alpha8 beta1 is critically important for epithelial-
 RT mesenchymal interactions during kidney morphogenesis.";
 RL Cell 88:603-613 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98217301; PubMed=9548928;
 RA Denda S., Muller U., Crossin K.L., Briceon H.P., Reichardt L.F.;
 RT "Utilization of a soluble integrin-alkaline phosphatase chimera to
 RT characterize integrin alpha 8 beta 1 receptor interactions with
 RT tenascin; murine alpha 8 beta 1 binds to the RGD site in tenascin-C
 RT fragments, but not to native tenascin-C";
 RL Biochemistry 37:5464-5474 (1998).
 DR EMBL; AF041409; AAC15665.1; -
 DR HSSP; P06756; IJUV2.

DR MGI:109442; Itga8.
 DR GO; GO:0008305; C:integrin complex; IEA.
 DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
 DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF01839; FG-GAP; 4.
 DR Pfam; PF00357; Integrin_A; 1.
 DR PRINTS; PR01185; INTEGRIN_A.
 DR SMART; SM00191; Int_alpha; 5.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 FT NON_TER 1
 SQ SEQUENCE 1012 AA; 112384 MW; 2A535AEC3867581 CRC64;
 Query Match 8.8%; Score 96.5; DB 11; Length 1012;
 Best Local Similarity 22.0%; Pred. No. 0.43;
 Matches 37; Conservative 32; Mismatches 40; Indels 59; Gaps 8;
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 DB 896 GGSAY--LKVRSRLWAHTFLKRNNDHYALASLVSEVKMPYKE----- 938
 QY 80 RVSEFWVTDPSPKNTLPA--VEVQSAIRMNKNRINNNAFFLNDQTLFLKIPSTLAPPMD 137
 DB 939 -----QPAK--LPAGSTAVKTSV-----IWAT--PNVS 962
 QY 138 PSVFIMIIIFGVIFCIIIVAILLIL--SGIWORRRKNKEPSEVDDAE 183
 DB 963 PSIFLWVILAILLGLLVAILTLALWKCGFFDRARPPQD--EMTDRE 1008
 RESULT 15
 Q9W6V5
 ID Q9W6V5 PRELIMINARY; PRT; 1406 AA.
 AC Q9W6V5;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 D3 Supporting-cell antigen precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=99296852; PubMed=10366616;
 RA Kruger R.P., Goodyear R.J., Legan P.K., Warchol M., Raphael Y.,
 RA Cotanche D.A., Richardson G.P.;
 RT "The supporting-cell antigen: a receptor-like protein tyrosine
 RT phosphatase expressed in the sensory epithelia of the inner ear.";
 RL J. Neurosci. 19:4815-4827 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RA Legan P.K.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ238216; CAB41885.2; -
 DR HSSP; P18052; 1VPO.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_pp.
 DR Pfam; PF00041; fn3; 9.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PTRYPHPTASE.
 DR SMART; SM00060; FN3; 9.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

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DR PROSITE; PSS0056; TYR_PHOSPHATASE.2; 1.
DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 1406 AA; 2D609885CC0F367B CRC64;

Query Match      8.7%; Score 95.5; DB 13; Length 1406;
Best Local Similarity 25.4%; Pred. No. 0.81;
Matches 31; Conservative 22; Mismatches 50; Indels 21; Gaps 4;

QY 87 VTDPSKNHTLPAVEVOSAIRMKNRINNAPFLN-----DQTLFLKIPSTLAP 134
   : : : : : : : : : : : : : : : : : : : :
Db 976 IVDVGKNTMGYENGPLIPLHYSRASVAGTINFTVANKMQEYSVSPSCSEWSL 1035

QY 135 PNDPSYPVIMIIIFGVFCIIIVAILLGS--INQRRRNKKEPSVEDDAEDKCE--NMI 190
   : : : : : : : : : : : : : : : : : : : :
Db 1036 PQDPGV-----IAGAVIGCULAILVAVIGCYIFWRRRRADKKNTEVSPFKIKSKMI 1090

QY 191 TIEN 194
   : :
Db 1091 KVEN 1094

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Search completed: April 1, 2004, 16:27:53
Job time : 47 secs